

STIC-Biotech/ChemLib

85648

From: Fredman, Jeffrey
Sent: Thursday, January 30, 2003 1:46 PM
To: STIC-Biotech/ChemLib
Cc: Angell, Jon E
Subject: FW: RUSH Sequence Database Search Request

RECEIVED

JAN 30 2003

(STIC)

PLEASE RUSH.

I Approve.

Jeff Fredman

-----Original Message-----

From: Angell, Jon E
Sent: Thursday, January 30, 2003 12:20 PM
To: Fredman, Jeffrey
Subject: RUSH Sequence Database Search Request

SEARCH REQUEST FORM
Scientific and Technical Information Center

Examiner# : 78697
Art Unit : 1635
Phone Number: 605-1165
Date: 1/30/03
Serial Number: 09/622,846
MailBox & Bldg/Room Location: CM1-11E12
Results Format Preferred (circle): Paper

I would like to have a standard search and please include all pending databases performed using the following SEQ. ID NOs. from application : 09/622,846

SEQ ID NO. 16--nucleic acid about 2400 nucleotides long

Thanks,
Eric

J. Eric Angell
Art Unit 1635
CM1 12D15
703-605-1165
mailbox CM1 11E12

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

Searcher: Jan
Phone: 4456
Location: _____
Date Picked Up: 1/30/03
Date Completed: 1/31/03
Searcher Prep/Review: _____
Clerical: W
Online time: 10

TYPE OF SEARCH: ☒
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: ☒
WWW/Internet: _____
Other (specify): _____

Gencore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 20:58:43 ; Search time 6122 Seconds
(without alignments)
11608.796 Million cell updates/sec

Title: us-09-622-846-16

Perfect score: 2442
Sequence: 1 taccctccagctccgagtc.....ttgttcacgtccctcttg 2442

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hgt: *
3: gb_in: *
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8: gb_pl: *
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10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vt: *
15: em_da: *
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24: em_pi: *
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26: em_ro: *
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28: em_un: *
29: em_vt: *
30: em_hgt_hum: *
31: em_hgt_inv: *
32: em_hgt_other: *
33: em_hgt_mus: *
34: em_hgt_pin: *
35: em_hgt_rtd: *
36: em_hgt_mam: *
37: em_hgt_vrt: *
38: em_sy: *
39: em_hgt_hum: *
40: em_hgt_mus: *
41: em_hgt_other: *

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2442	100.0	2442	6	AX018772	AX018772 Sequence
2	2440.4	99.9	2442	6	AX018773	AX018773 Sequence
3	2420	99.1	2441	6	AX018774	AX018774 Sequence
4	2420	99.1	4361	9	HUMH6	J03027 Human MHC C
5	2418.4	99.0	2441	6	AX018775	AX018775 Sequence
6	2399.8	98.3	5589	9	AF523304	AF523304 Homo sapi
7	2399.6	98.3	3640	9	S50740	S50740 HLA-G (7.0E
8	2395.4	98.1	38194	9	AC004193	AC004193 Homo sapi
9	2395.4	98.1	93937	9	AL645929	AL645929 Human DNA
10	2395.4	98.1	148834	9	HS377H14	AL022723 Human DNA
11	2393.8	98.0	5577	9	AF523301	AF523301 Homo sapi
12	2393.8	98.0	5577	9	AF523302	AF523302 Homo sapi
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18	2373.4	97.2	81561	9	AB023057	AB023057 Homo sapi
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20	2373.4	97.2	105633	9	AL671561	AL671561 Human DNA
21	2373.4	97.1	129818	9	AP000521	AP000521 Homo sapi
22	2371.8	97.1	5588	9	AF523303	AF523303 Homo sapi
23	2370.2	96.7	319486	9	AF055066	AF055066 Homo sapi
24	2361.4	96.7	5587	9	AF523299	AF523299 Homo sapi
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ALIGNMENTS

RESULT 1
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LOCUS AX018772 2442 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 16 from Patent WO9943851.
ACCESSION AX018772
VERSION AX018772.1 GI:10042894
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 2442)
Mccarthy,T.V., Bermingham,J., Jenkins,D.M., O and Quane,K.A.
TITLE Hla linked pre-eclampsia and miscarriage susceptibility gene
JOURNAL Patent: WO 9943851-A 16 02-SEP-1999;

Pred. No. is the number of results predicted by chance to have a

MCCARTHY TOMMIE V (IE); BIRMINGHAM JOHN (IE); JENKINS DAVID M (IE);
BRIEN MARGARET O (IE); NAT UNIVERSITY OF IRELAND CORK (IE); QUANE
KATHLEEN A (IE)

FEATURES
Source Location/Qualifiers
1..2442

/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 485 a 659 c 735 g 563 t
ORIGIN

Query Match 100.0%; Score 2442; DB 6; Length 2442;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TACTCCGAGTCTCCGGGCTGCGATCCACCCGAGGCCGCGGAGACCCGCGCAGACCTTC 60
DB 1 TACTCCGAGTCTCCGGGCTGCGATCCACCCGAGGCCGCGGAGACCCGCGCAGACCTTC 60
OY 61 TACCTGGAGAACCCCAAGGCGGCTTTACCAAAATCCCGGGGTGGGTCCGGGCGAGGG 120
DB 61 TACCTGGAGAACCCCAAGGCGGCTTTACCAAAATCCCGGGGTGGGTCCGGGCGAGGG 120
OY 121 CGAGGCTGCTGGGCGGGGCTGACCGAGGGGGTGGGCGAGTTCTCACACCCCTCCAGTG 180
DB 121 CGAGGCTGCTGGGCGGGGCTGACCGAGGGGGTGGGCGAGTTCTCACACCCCTCCAGTG 180
OY 181 GATGATTTGGCTGCGACCTGGGGTCCGAGCGACGCTCTCCGGGGTATGACAGATATGC 240
DB 181 GATGATTTGGCTGCGACCTGGGGTCCGAGCGACGCTCTCCGGGGTATGACAGATATGC 240
OY 241 CTACATGGGCAAGATTTACCTCGCCCTGAAGAGACCTCGGCTCTCGAGCCGACGCGA 300
DB 241 CTACATGGGCAAGATTTACCTCGCCCTGAAGAGACCTCGGCTCTCGAGCCGACGCGA 300
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DB 301 CACTCGGCTCAGATCTCCAAAGCCCAAGTGTGAGCGGCCCAATGTGCTTAACAAGAGAG 360
OY 361 AACCCTACCTGGAGGCGACGTGCGAGTGGCTCCACAGATACCTGGAGAGCGGAAGA 420
DB 361 AACCCTACCTGGAGGCGACGTGCGAGTGGCTCCACAGATACCTGGAGAGCGGAAGA 420
OY 421 GATGCTGAGGCGCGGGGTACCAAGGGCAGTGGGGCGCTCTGATCTCTGTAGACT 480
DB 421 GATGCTGAGGCGCGGGGTACCAAGGGCAGTGGGGCGCTCTGATCTCTGTAGACT 480
OY 481 CTGACCTGGCTACACAGAGAGAGAGAAATGGACCAACTAGAGATTCGCGCT 540
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DB 1141 CAGCGGAGTGGGAGAGACCAAGACCGAGAGTGGAGCTGGAGACCAAGGCTGAGGG 1200
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OY 1381 GGTGGTGTGAGAGGCTGGGGGCTCAGAGACCTCACCCTTCACTCTTCCAGAGCACT 1440
DB 1381 GGTGGTGTGAGAGGCTGGGGGCTCAGAGACCTCACCCTTCACTCTTCCAGAGCACT 1440
OY 1441 CTTCCCTGCCCCACCATCCCATCATGAGGTATCGTCTGAGGCTGTGCTTGGACGTG 1500
DB 1441 CTTCCCTGCCCCACCATCCCATCATGAGGTATCGTCTGAGGCTGTGCTTGGACGTG 1500
OY 1501 TAGTACCTGAGAGCTGCGGTGCTGTGCTGTGAGAGAGAGAGAGACCTAGATAGAGAG 1560
DB 1501 TAGTACCTGAGAGCTGCGGTGCTGTGCTGTGAGAGAGAGAGAGACCTAGATAGAGAG 1560
OY 1561 GGGTGAACAAGTGGGGTCTGAGTTTCTTCCACAGGGGGTTTCAAGCCCGAGTAGAA 1620
DB 1561 GGGTGAACAAGTGGGGTCTGAGTTTCTTCCACAGGGGGTTTCAAGCCCGAGTAGAA 1620
OY 1621 GTTGCCCTGCTGCTTACGTAGGAGACCATTCACATCTATGAGGCTTCCACGCTTGG 1680
DB 1621 GTTGCCCTGCTGCTTACGTAGGAGACCATTCACATCTATGAGGCTTCCACGCTTGG 1680
OY 1681 CCCTGTGAGCAGACCTTCTCTTTGTAAGACCTGTGACAAATGAGAGACATTTAT 1740
DB 1681 CCCTGTGAGCAGACCTTCTCTTTGTAAGACCTGTGACAAATGAGAGACATTTAT 1740
OY 1741 TACTTGTATTTAGTATGATGGGACCTGATCCAGTAATTCACAGGTACAGAGAGTTC 1800
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OY 1921 GACTAGAGAGTCTCTTGAAGACCTCATAGGCTCTGACACCTTCTGAGCTCTCAAGAGCA 1980
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Db 2401 GTGTGGGAGTGAAGTATTTGTTTCATGCTTCCCTTTG 2442

RESULT 2
AX018773 2442 bp DNA linear PAT 07-SEP-2000
LOCUS AX018773
DEFINITION Sequence 17 from Patent WO943851.
ACCESSION AX018773
VERSION AX018773.1 GI:10042895
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2442)
McCarthy,T.V., Bermingham,J., Jenkins,D.M., O and Quane,K.A.
Hla linked pre-eclampsia and miscarriage susceptibility gene
Patent: WO 943851-A 17 02-SEP-1999;
MCCARTHY TOMMIE V (IE); BERMINGHAM JOHN (IE); JENKINS DAVID M (IE);
BRIEN MARGARET O (IE); NAT UNIVERSITY OF IRELAND CORK (IE); QUANE
KATHLEEN A (IE)

FEATURES
source location/Qualifiers
1..2442

BASE COUNT 485 a 658 c 735 g 564 t
ORIGIN

Query Match 99.9%; Score 2440.4; DB 6; Length 2442;

Best Local Similarity 100.0%; Pred.No. 0;
Matches 2441; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 841 CCCCCCTCAGAGACAGAACTTCCAGGAATGAGAGATTTCCAGAGTCCCGGCTGTC 900
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Db 1081 GAGGCAACCTGAGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
QY 1141 CAGCGGATGAGGAGAGCAAGACCAAGAGAGTGAAGTCTGTGAGACAGGCGCTGAGG 1200
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LOCUS	AX018774	2441 bp	DNA linear
DEFINITION	Sequence 18 from Patent WO9943851.		
ACCESSION	AX018774		
VERSION	AX018774.1	GI:10042896	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	McCarthy,T.V., Bermingham,J., Jenkins,D.M., O and Quane,K.A.		
TITLE	Hla linked pre-eclampsia and miscarriage susceptibility gene		
JOURNAL	Patent: WO 9943851-A 18 02-SEP-1999; MCCARTHY TOMMIE V (IE); BERMINGHAM JOHN (IE); JENKINS DAVID M (IE); BRIEN MARGARET O (IE); NAT UNIVERSITY OF IRELAND CORK (IE); QUANE KATHLEEN A (IE)		
FEATURES	Location/Qualifiers		
Source	1..2441		
BASE COUNT	488 a 659 c 735 g 559 t		
ORIGIN			
Query Match	99.1%; Score 2420; DB 6; Length 2441;		
Best Local Similarity	100.0%; Pred. No. 0;		
Matches 2420; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
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Qy	61	TACCTGGAGAACCCCAAGGCGCTTTTACCAAAATCCCGCGGGTGGGTCGCGGAGAGG	120
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Qy	121	CGAGGCTGGTGGGCGGCTGACCGAGGGGTGGGCGCAGGTTCTCAACCTCCAGTG	180
Db	121	CGAGGCTGGTGGGCGGCTGACCGAGGGGTGGGCGCAGGTTCTCAACCTCCAGTG	180
Qy	181	GATGATTTGGTCGACGCTGGGGTCCGAGGAGCGCTCTCCCGGGGTGTGAACAATATGC	240
Db	181	GATGATTTGGTCGACGCTGGGGTCCGAGGAGCGCTCTCTCCCGGGGTGTGAACAATATGC	240
Qy	241	CTACGATGGCAAGATTAATCTCGCCTCAAGAGAGACTCGCTCTGGACCGAGCGGA	300
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Qy	301	CACATGGGCTCAGATCTCCAAAGCGCAATGTGAGCGGCCATATGTGCTGAACAAAGAG	360
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Qy	361	AGCCCTACTGGAGGCGAGTGCCTGAGATGGCTCACAGATTAATCTGGAGAACGGGAAGA	420
Db	361	AGCCCTACTGGAGGCGAGTGCCTGAGATGGCTCACAGATTAATCTGGAGAACGGGAAGA	420
Qy	421	GATGCTGACGCGCGGGTACACAGGGGAGTGGGGCGCTCTCGATCTCTGTAGACT	480
Db	421	GATGCTGACGCGCGGGTACACAGGGGAGTGGGGCGCTCTCGATCTCTGTAGACT	480
Qy	481	CTCAGCTGGCCTTAGCACAGAGAGAGAAATGGGACCAACACTAGAAATATGCCT	540
Db	481	CTCAGCTGGCCTTAGCACAGAGAGAGAGAAATGGGACCAACACTAGAAATATGCCT	540

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 Db 601 TTCTGAGGCCCCCTCTCTCTCTGAGCAATTAAAGGATGAAGTCTCTGAGGAGTGA 660
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 Db 2401 GTGTGGACTGATGGCAAG 2420

RESULT 4
 HUMH6
 LOCUS 4361 bp DNA linear PRI 02-MAY-1996
 DEFINITION Human MHC class I HLA-6.09 gene, complete cds.
 ACCESSION J03027
 VERSION 1
 KEYWORDS cell surface antigen; cell surface glycoprotein; class I gene; major histocompatibility complex.
 SOURCE Homo sapiens (clone: HLA6.0.) DNA.
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 4361)
 AUTHORS Geraghty,D.E., Koller,B.H. and Orr,R.T.
 TITLE A human major histocompatibility complex class I gene that encodes a protein with a shortened cytoplasmic segment
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9145-9149 (1987)

FEATURES	source
MEDLINE PUBMED COMMENT	88097444 3480534 Draft entry and computer-readable sequence for [1] kindly provided by H.T.Orr, 22-SEP-1987.
location/Qualifiers	1..4361
organism	"Homo sapiens"
db_xref	"taxon:9606"
clone	"HLA6.0."
cell_line	"#721.144"
cell_type	"lymphoblast"
gene	680..4038
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gene	/gene="MHC_HLA-6.09"
note	"putative"
number	1
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intron	/gene="MHC_HLA-6.09" /number=6 3347..3487
exon	/gene="MHC_HLA-6.09" /number=6 3488..3535

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Dp	2160	CCCCCGCTCAGAACTAGAACTTTTCCAAAGAAATAGAGAAATTATCCAGTGCCTCGTGTCC	2219
QY	901	AGCCTGGTGTCTGGGTTCTGTGCTCCCTTCCCAACCAGTATCTGGTTCACTCTTAGG	960
Dp	2220	AGCCTGGTGTCTGGGTTCTGTGCTCCCTTCCCAACCAGTATCTGGTTCACTCTTAGG	2279
QY	961	ATGGTACATCCAGGTGCTGTGAGTAGTCCCATAGAGATGACAAATGCTTGAAATTTTC	1020
Dp	2280	ATGGTACATCCAGGTGCTGTGAGTAGTCCCATAGAGATGACAAATGCTTGAAATTTTC	2339
QY	1021	TGACTTCTCTTTCAGACCCCTCCCAAGACACAGTACCCACACCCCTGTCTTGACTAT	1080
Dp	2340	TGACTTCTCTTTCAGACCCCTCCCAAGACACAGTACCCACACCCCTGTCTTGACTAT	2399
QY	1081	GAGGCCACCTGAGGTGCTTGGGCTCTTACCCCTGGGAGATCATAGCACTGG	1140
Dp	2400	GAGGCCACCTGAGGTGCTTGGGCTCTTACCCCTGGGAGATCATAGCACTGG	2459
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Dp	2460	CAGGGGATGGGAGAGACCAAGACCAGACCTGAGACTGTGAGAACAGGCTGCAGG	2519
QY	1201	GATGGAACCTTCAGAACTGGGGCACTGTGTGTGTCCTTCTGAGAGAGACAGATAC	1260
Dp	2520	GATGGAACCTTCAGAACTGGGGCACTGTGTGTGTCCTTCTGAGAGAGACAGATAC	2579
QY	1261	ACGTGCATGTGCAGCATGAGGGGCTGCGGAGGCCCTCATGTCTGATGATGAGTAAAGAG	1320
Dp	2580	ACGTGCATGTGCAGCATGAGGGGCTGCGGAGGCCCTCATGTCTGATGATGAGTAAAGAG	2639
QY	1321	GGAAATGAGAGGCAATCATGTCTGTATAGGAAACAGAGAGCTCTCGAAGACTTTAACAG	1380
Dp	2640	GGAAATGAGAGGCAATCATGTCTGTATAGGAAACAGAGAGCTCTCGAAGACTTTAACAG	2699
QY	1381	GGTGTGTGTGAGGGGCTGGGGGTCAGAGACCTTCACCTTCCTTCCAGAGCAGT	1440
Dp	2700	GGTGTGTGTGAGGGGCTGGGGGTCAGAGACCTTCACCTTCCTTCCAGAGCAGT	2759
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Dp	2760	CTTCCCTGCCACCATATCCCATATAGGGTATGTGTTCTGTGGCTGGTTCTTGACACTG	2819
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QY	1621	GTGTGCTGCTGCTGTACTGTAGGAGACACATACACTCATAGGGCTTACCAGCTGGG	1680
Dp	2940	GTGTGCTGCTGCTGTACTGTAGGAGACACATACACTCATAGGGCTTACCAGCTGGG	2999
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Dp	3000	CCCTGTGGCCAGACCTCTCTTTTGTAAAGACCTGTGACAAATGAAGGACAGATTAT	3059
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Dp	3060	TACCTTGATGATTTAGTGAATGGGACCTTATCCAGTATCACAGGTACAGAGAAAGTC	3119
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Dp	3120	CCTGCTAAGGACAGACCTTAGAGAGGCAATGGTGCAGAGACCCACATCTGCTTCTTG	3179
QY	1861	TTTTTTCAGTACGCCCTGGGCTGTCACTACACTTTTGTGAAATCTTTCAGGGCTCAA	1920
Dp	3180	TTTTTTCAGTACGCCCTGGGCTGTGTCACTACACTTTTGTGAAATCTTTCAGGGCTCAA	3239
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Db	3240	GACTAGGAGGTTCCCTTAGCACTCTATAGCCCTGACACTTTCTTGCCCTCTCACAGACA	3299
Qy	1981	TTTTTCTTCCACAGATTGAAAAGGAGGAGCTACTCTCAGCCTGCAGTAATGATGAAG	2040
Db	3300	TTTTTCTTCCCAAGATTGAAGAAGGAGGAGCTACTCTCAGCCTGCAGTAATGATGAAG	3359
Qy	2011	AGGCTGATCCCTGAGATCCCTTGGAATCTTGTGTGTTGGAGCCATGGGGAGACCTACCCAC	2100
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DEFINITION	Sequence 19 from Patent WO9943851.				
ACCESSION	AX018775				
VERSION	AX018775.1	GI:10042897			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
REFERENCE	1 (bases 1 to 2441)				
AUTHORS	McCarthy,T.V., Bermingham,J., Jenkins,D.M., O and Quane,K.A.				
TITLE	Hla linked pre-eclampsia and miscarriage susceptibility gene				
JOURNAL	Patent: WO 9943851-A 19 02-SEP-1999; MCCARTHY TOMMIE V (IE); BERMINGHAM JOHN (IE); JENKINS DAVID M (IE); BRINN MARGARET O (IE); NAT UNIVERSITY OF IRELAND CORK (IE); QUANE KATHLEEN A (IE)				
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LOCUS Homo sapiens clone M714 MHC class Ib antigen (HLA-G) gene,
DEFINITION HLA-G*01016 allele, complete cds.
ACCESSION AF523304
VERSION AF523304.1 GI:21686649
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 5589)
AUTHORS Ishitani,A., Miki,A., Williams,L.M., Moore,Y. and Geraghty,D.E.
TITLE HLA-E, F, and G polymorphism: genomic sequence defines new
variation spanning the nonclassical class I genes
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 5589)
AUTHORS Ishitani,A., Miki,A., Williams,L.M., Moore,Y. and Geraghty,D.E.
TITLE Direct Submission
JOURNAL Submitted (21-JUN-2002) Clinical Division, Fred Hutchinson Cancer
Research Center, 1100 Fairview Ave. N., D4-100, Seattle, WA
98109-1024, USA

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VERSION	S50740.1	GI:259087	
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ORGANISM	Homo sapiens		
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AUTHORS	Tamaki, J.		
TITLE	Analysis of polymorphism at the human class I MHC locus, HLA-G		
JOURNAL	Hokkaido Igaku Zasshi 67 (5), 583-594 (1992)		
MEDLINE	93051989		
PUBMED	1427601		
REMARK	Genbank staff at the National Library of Medicine created this entry [NCBI gi dbseq 120998] from the original journal article. This sequence comes from Fig. 5.		
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LOCUS

DEFINITION Homo sapiens clone UWGC:Y23c142 from 6p21, complete sequence.
AC004193
VERSION AC004193.1 GI:3980471
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SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 38194)
AUTHORS Janer M., Guillaudoux T., Vu Q., Kuyavin T., Harter H. and
Geraghty D.E.
TITLE Large scale sequence analysis of the human MHC class I region
JOURNAL Unpublished (1998)
REMARK Fred Hutchinson Cancer Research Center
The Clinical Research Division
1100 Fairview Ave. N., P.O. Box 19024
Seattle, WA 98109-1024
2 (bases 1 to 38194)
Geraghty, D.E. and Olson, M.V.
REFERENCE Direct Submission
AUTHORS Submitted (23-FEB-1998) Human Genome Center, University of
TITLE Washington, Box 352145, Seattle, WA 98195, USA
JOURNAL 3 (bases 1 to 38194)
Geraghty, D.E. and Olson, M.V.
REFERENCE Direct Submission
AUTHORS Submitted (08-DEC-1998) Human Genome Center, University of
TITLE Washington, Box 352145, Seattle, WA 98195, USA
JOURNAL University of Washington Human Genome Center
Box 352145 Seattle, WA 98195
REMARK Contact: Daniel E. Geraghty (geraghty@fhcrc.org)
On Dec 8, 1998 this sequence version replaced gi:2905867.
Overlapping Sequences:
5': UWGC:Y23C022 (Genbank Accession: AC004194)
3': UWGC:Y23X010 (Genbank Accession: AC004172)

Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
Genbank flat file format but are available as part
of this entry's ASN.1 file.

Double stranded (DS) coverage: 90.7%
DS or two chemistry coverage: 100.0%
Single stranded regions: 0

Sequence Validation:
This sequence has been validated by Multiple Complete Digest
Mapping. Comparison of the experimentally derived map digest
fragments with sequence-predicted fragments is given below.
Small fragments below a variable cutoff (approximately 400-600bp)
are not mapped and hence do not appear in the table. There are no
significant remaining discrepancies between the experimental and
predicted values. Uniquely ordered fragment groups are separated
by dashed lines.

Map BgIII Seq HindIII Seq NsiI Seq

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6992.92 6962.00 2803.45 2806.00 2697.65 2688.00

2418.71 2395.00 5412.37 5370.00 5391.17 5365.00

1445.83 1463.00 7334.90 7251.00 1767.38 1763.00

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source

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ORIGIN

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Best Local Similarity 99.8% Pred. No. 0;
Matches 2419; Conservative 0; Mismatches 1; Indels 3; Gaps 2;

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RESULT 9
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1
REFERENCE
AUTHORS Griffiths, C.
TITLE Direct Submision
JOURNAL Submitted (23-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk
Clome requests: clomequests@sanger.ac.uk
On Jan 6, 2002 this sequence version replaced gi:11736625.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em, EMBL; SW,
SWISSPROT; Tr, TrEMBL; Wp, WormPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
Xxbac-1216 is
from a CHORI-501 human bac - PGF cell line library VECTOR:
PTARPA2.1
This sequence was generated from part of bacterial clone contigs
constructed by the MHC Haplotype Consortium and collaborators.
Further information can be found at
http://www.sanger.ac.uk/HGP/Chf6/MHC.
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RESULT 10
HS377H14/c
LOCUS
DEFINITION
Human DNA sequence from clone RP3-377H14 on chromosome 6p21.32-22.1. Contains the HLA-G gene for major histocompatibility complex class I G (HLA 6.0) an MHC class I pseudogene, an RPL7A (60S Ribosomal Protein L7A) pseudogene, a gene for a novel MHC class I protein, an interferon-inducible protein 1-80 pseudogene, an RPL23A (60S Ribosomal Protein L23A) pseudogene, an HCGIX pseudogene, an MICB or PERB1.1 pseudogene, the HLA-F gene for major histocompatibility complex class I F (CD142), and four p5-1 pseudogenes. Contains EST, STSs, GSS and six CpG islands, complete sequence.

AL022723 GI:5002624
VERSION
HTG: CDA12; CpG island; HCGIX; HLA-F; HLA-G; MICB; P5-1;
KEYWORDS
PERB1.1; RPL23A; RPL7A.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 148834)
AUTHORS
Williams,S.
TITLE
Direct Submission
JOURNAL

COMMENT
Submitted (29-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
On Jun 7, 1999 this sequence version replaced gi:4757010.
This sequence was generated from part of bacterial clone configs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group in collaboration with Armin Volz and Andreas Ziegler.
Further information can be found at
http://www.sanger.ac.uk/HGP/Ch6
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
RP3-377H14 is from the library RPi-3 constructed by the group of Pieter de Jong.

For further details see
<http://www.chori.org/bacpac/home.htm>
VECTOR: PCYPAC2

FEATURES
This sequence is the entire insert of clone RP3-377H14.
Location/Qualifiers

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RESULT 11
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VERSION AF523301.1 GI:21686643
KEYWORDS human.
SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 5577)
AUTHORS Ishihara, A., Miki, A., Williams, L.M., Moore, Y., and Geraghty, D.E.
TITLE HLA-E, F, and G polymorphism: genomic sequence defines new
variation spanning the nonclassical class I genes
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 5577)
AUTHORS Ishihara, A., Miki, A., Williams, L.M., Moore, Y., and Geraghty, D.E.
TITLE Direct Submission
JOURNAL Submitted (21-JUN-2002) Clinical Division, Fred Hutchinson Cancer
Research Center, 1100 Fairview Ave. N., D4-100, Seattle, WA
98109-1024, USA
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Best Local Similarity 99.8%; Pred. No. 0;
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AF523302
ACCESSION
VERSION AF523302.1 GI:21686645
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 5577)
Ishitani,A., Miki,A., Williams,L.M., Moore,Y., and Geraghty,D.E.
HLA-E, F, and G polymorphism: genomic sequence defines new
variation spanning the nonclassical class I genes
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 5577)
Ishitani,A., Miki,A., Williams,L.M., Moore,Y., and Geraghty,D.E.
AUTHORS Direct Submission
TITLE Submitted (21-JUN-2002) Clinical Division, Fred Hutchinson Cancer
Research Center, 1100 Fairview Ave. N., D4-100, Seattle, WA
JOURNAL 98109-1024, USA
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QY	181	GATGATTTGGGTCGCGACCTCGGGGTCCGACGAGACGCTCTCTCGCGGGGTATGAACAGTATGC	240
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QY	1861	TTTTTCTCGAT--CGCCCTGGGCTGTG	AGATCACACATTTCTTGGAACCTTTCGAGGGTCC	1918	
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Db	3719	CATTTTCTTCCACAGATTGAAAAGAGGAGGAGTCACTCTCAGGCTGCAAGTAAGTATGAA	3778
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ACCESSION	HLA-G*01011 allele, complete cds.		
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SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 5574)		
JOURNAL	Ishitani,A., Miki,A., Williams,L.M., Moore,Y. and Geraghty,D.E.		
REFERENCE	HLA-E, F, and G polymorphism: genomic sequence defines new		
AUTHORS	variation spanning the nonclassical class I genes		
TITLE	Unpublished		
JOURNAL	2 (bases 1 to 5574)		
REFERENCE	Ishitani,A., Miki,A., Williams,L.M., Moore,Y. and Geraghty,D.E.		
AUTHORS	Direct Submission		
TITLE	Submitted (21-JUN-2002) Clinical Division, Fred Hutchinson Cancer		
JOURNAL	Research Center, 1100 Fairview Ave. N., D4-100, Seattle, WA		
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RESULT 14
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 HLA-G*01011 allele, complete cds.
 AF523305
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 1 (bases 1 to 5574)
 Ishihara, A., Miki, A., Williams, L.M., Moore, Y. and Gerghely, D.E.
 Variation spanning the nonclassical class I genes
 Unpublished
 2 (bases 1 to 5574)
 Ishihara, A., Miki, A., Williams, L.M., Moore, Y. and Gerghely, D.E.
 Direct Submission
 Submitted (21-JUN-2002) Clinical Division, Fred Hutchinson Cancer
 Research Center, 1100 Fairview Ave. N., D4-100, Seattle, WA
 98109-1024, USA

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BASE COUNT 1236 a 1438 c 1531 g 1364 t 5 others
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 2417; Conservative 0; Mismatches 3; Indels 3; Gaps 2;
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: Patent No. US20020137081A1
: GENERAL INFORMATION:
: APPLICANT: Olga Bandman
: TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
: FILE REFERENCE: PA-0028 US
: CURRENT APPLICATION NUMBER: US/10/044,090
: CURRENT FILING DATE: 2002-01-09
: NUMBER OF SEQ ID NOS: 850
: SOFTWARE: PERL Program
: SEQ ID NO 577
: LENGTH: 1389
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: incyle ID No. US20020137081A1 1382902.19
US-10-044-090-577

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; Sequence 562 Application US/10044090
; Patent No. US20020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 562
LENGTH: 1155
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 1383423.1
NAME/KEY: unsure
LOCATION: 344, 394
; OTHER INFORMATION: a, t, c, g, or other
US-10-044-090-562

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 2 CURRENT FILING DATE: 2001-05-23
 3 PRIOR APPLICATION NUMBER: US 60/180,312
 4 PRIOR FILING DATE: 2000-02-04
 5 PRIOR APPLICATION NUMBER: US 60/207,456
 6 PRIOR FILING DATE: 2000-05-26
 7 PRIOR APPLICATION NUMBER: US 09/632,366
 8 PRIOR FILING DATE: 2000-08-03
 9 PRIOR APPLICATION NUMBER: GB 24263,6
 10 PRIOR FILING DATE: 2000-10-04
 11 PRIOR APPLICATION NUMBER: US 60/236,359
 12 PRIOR FILING DATE: 2000-09-27
 13 PRIOR APPLICATION NUMBER: PCT/US01/00666
 14 PRIOR FILING DATE: 2001-01-30
 15 PRIOR APPLICATION NUMBER: PCT/US01/00667
 16 PRIOR FILING DATE: 2001-01-30
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 32 PRIOR FILING DATE: 2001-01-30
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 34 PRIOR FILING DATE: 2000-09-21
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 36 PRIOR FILING DATE: 2000-06-30

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RESULT 5
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: Sequence 738, Application US/09864761
: Patent No. US20020048763A1
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: GENERAL INFORMATION:
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: APPLICANT: Penn, Sharon G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
:
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
: TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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: FILE REFERENCE: Aeonica-X-1
:
: CURRENT APPLICATION NUMBER: US/09/864,761
:
: CURRENT FILING DATE: 2001-05-23
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; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 738
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AB023057.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2e+02
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1e+02
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 27
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 33
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 25
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 13
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 69
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 53
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.1e+02
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 18
US-09-864-761-738

Query Match          18.9%; Score 461.2; DB 10; Length 466;
Best Local Similarity 99.4%; Pred. No. 8.9e-124;
Matches 463; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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|||||
Db 286 GCGTCCGAGAGCCCTCATGCTAGATGAGTAAGAGGAGATGAGGACATCATGCTG 227
QY 1343 TTAGGGAAGACAGAGCCTCTCTGAAGACCTTTAACAGGCTGGTGTAGGCTGGGG 1402
Db 226 TTAGGGAAGACAGAGCCTCTCTGAAGACCTTTAACAGGCTGGTGTAGGCTGGGG 167
QY 1403 TCAGAGACCTCATGCTACCTCTTCCAGAGCAGTCTCCCTCCACCATCCCAT 1462
Db 166 TCAGAGACCTCATGCTACCTCTTCCAGAGCAGTCTCCCTCCACCATCCCAT 107
QY 1463 CATGGATATGCTGTGAGCCTGCTGCTCTTCCAGCTGTAGTCACTGAGCTGCGTGC 1522
Db 106 CATGGATATGCTGTGAGCCTGCTGCTCTTCCAGCTGTAGTCACTGAGCTGCGTGC 47
QY 1523 TCCTGTCTGTGAGGAAGAGAGCTCAGTAAAGAGGGGTACA 1568
Db 46 TCCTGTCTGTGAGGAAGAGAGCTCAGTAAAGAGGGGTGACA 1

RESULT 6
US-09-964-261-396
; Sequence 396, Application US/09964261
; Publication No. US20020197613A1
; GENERAL INFORMATION:
; APPLICANT: De Canck, Ilse
; APPLICANT: Rombout, Annelies
; APPLICANT: Rossau, Rudi
; TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES
; FILE REFERENCE: IGJ-002
; CURRENT APPLICATION NUMBER: US/09/964,261
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: EP 99870068.6
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/138,614
; PRIOR FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 396
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-261-396

Query Match          17.6%; Score 429.2; DB 9; Length 600;
Best Local Similarity 86.4%; Pred. No. 1.9e-114;
Matches 522; Conservative 0; Mismatches 73; Indels 9; Gaps 4;
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||||| 360 TTCTAGTCCCTCAGCCCTCCACTGAGTCAGACAGAGTGGTGTCCCTC-TTCAGG 418
||||| 853 GACTAGAACTTCCAGAGAAATAGAGATTTATCCAGGTGCCCTGTCCAGCTGTGTCT 912
||||| 419 GACTAGAAATTTCCAGGAAATAGAGATTTATCCAGGTGCCCTGTGTCCAGCTGTGTCT 478
QY 913 GGGTCTGTGTCTCCCTTCCCAAGGATATCTGTATCTTCTTATGATGTGTATCC 972
Db 479 GGGTCTGTGTCTCCCTTCCCAAGGATATCTGTATCTTCTTATGATGTGTATCC 536
QY 973 AGGTCTGTGTCTCCCTTCCCAAGGATATCTGTATCTTCTTATGATGTGTATCC 1032
Db 537 GTGTCTGTGTCTCCCTTCCCAAGGATATCTGTATCTTCTTATGATGTGTATCC 596
QY 1033 TCAG 1036
Db 597 ACAG 600
```

RESULT 7

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US-09-964-261-407
; Sequence 407, Application US/09964261
; Publication No. US20020197613A1
; GENERAL INFORMATION:
; APPLICANT: De Canck, Ilse
; APPLICANT: Rombout, Annelies
; APPLICANT: Rossau, Rudi
; TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES
; FILE REFERENCE: 1G3-002
; CURRENT APPLICATION NUMBER: US/09/964, 261
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: EP 99870068.6
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/138,614
; PRIOR FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 407
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-261-407
```

Query Match 17.6%; Score 429.2; DB 9; Length 600;
Best Local Similarity 86.4%; Pred. No. 1.9e-114;
Matches 522; Conservative 0; Mismatches 73; Indels 9; Gaps 4;

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QY 438 GTACAGGGGAGAGTGGGGGCTCCCTGATCTCTGTAGACCTCTCAGCCTGGCTAGCA 497
Db 1 GTACAGGGGAGAGTGGGGGCTCCCTGATCTCTGTAGACCTCTCAGCCTGGCTAGCA 60
QY 498 CAAGAGAGAGAGAAATAGGAGCAACACTAGATATCGCCCTCTCTGTGTCTGTAGG 557
Db 61 CAAGAGAGAGAGAAATAGGAGCAACACTAGATATCGCCCTCTCTGTGTCTGTAGG 120
QY 558 AGAGAAATCTCTCTGGGTTTCCAGATCTGTAGCAGAGAGATCTGTAGGAGGCTGTCT 617
Db 121 AGAGAAATCTCTCTGGGTTTCCAGATCTGTAGCAGAGAGATCTGTAGGAGGCTGTCT 180
QY 618 GCTCTGTGGCAATTAAGGATGATCTGTAGGAGAGTGGAGGAGAAACAATCCCTG 677
Db 181 GCTCTGTGGCAATTAAGGATGATCTGTAGGAGAGTGGAGGAGAAACAATCCCTG 239
QY 678 GAAGACTATCAGGGGTTCCCTTTGAC-----CCACAGCAGCCTTGTGGACAGGACTTT 732
Db 240 GAATACTATGATGATGTTCCCTTTGACACACACAGCAGCAGCCTTGTGGAGCTTT 299
QY 733 TCCCTCAGAGCCTTGTCTGTCTGACACTCAATGTGTGTGGGGGTCTGACCTCAGCTC 792
Db 300 TCCCTCAGAGCCTTGTCTGTCTGACACTCAATGTGTGTGGGGGTCTGACCTCAGCTC 359
QY 793 CTCTGAGTCCCTTGGCTCCACTGAGTCAAGTCAAGACCGGAGGTCCCTGCTCCCGCTCAGA 852
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```
||||| 360 TTCTAGTCCCTCAGCCCTCCACTGAGTCAGACAGAGTGGTGTCCCTC-TTCAGG 418
||||| 853 GACTAGAACTTCCAGAGAAATAGAGATTTATCCAGGTGCCCTGTCCAGCTGTGTCT 912
||||| 419 GACTAGAAATTTCCAGGAAATAGAGATTTATCCAGGTGCCCTGTGTCCAGCTGTGTCT 478
QY 913 GGGTCTGTGTCTCCCTTCCCAAGGATATCTGTATCTTCTTATGATGTGTATCC 972
Db 479 GGGTCTGTGTCTCCCTTCCCAAGGATATCTGTATCTTCTTATGATGTGTATCC 536
QY 973 AGGTCTGTGTCTCCCTTCCCAAGGATATCTGTATCTTCTTATGATGTGTATCC 1032
Db 537 GTGTCTGTGTCTCCCTTCCCAAGGATATCTGTATCTTCTTATGATGTGTATCC 596
QY 1033 TCAG 1036
Db 597 ACAG 600
```

RESULT 8

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US-09-964-261-397
; Sequence 397, Application US/09964261
; Publication No. US20020197613A1
; GENERAL INFORMATION:
; APPLICANT: De Canck, Ilse
; APPLICANT: Rombout, Annelies
; APPLICANT: Rossau, Rudi
; TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES
; FILE REFERENCE: 1G3-002
; CURRENT APPLICATION NUMBER: US/09/964, 261
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: EP 99870068.6
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/138,614
; PRIOR FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 397
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-261-397
```

Query Match 17.5%; Score 427.6; DB 9; Length 600;
Best Local Similarity 86.3%; Pred. No. 5.7e-114;
Matches 521; Conservative 0; Mismatches 74; Indels 9; Gaps 4;

```
QY 438 GTACAGGGGAGAGTGGGGGCTCCCTGATCTCTGTAGACCTCTCAGCCTGGCTAGCA 497
Db 1 GTACAGGGGAGAGTGGGGGCTCCCTGATCTCTGTAGACCTCTCAGCCTGGCTAGCA 60
QY 498 CAAGAGAGAGAGAAATAGGAGCAACACTAGATATCGCCCTCTCTGTGTCTGTAGG 557
Db 61 CAAGAGAGAGAGAAATAGGAGCAACACTAGATATCGCCCTCTCTGTGTCTGTAGG 120
QY 558 AGAGAAATCTCTCTGGGTTTCCAGATCTGTAGCAGAGAGATCTGTAGGAGGCTGTCT 617
Db 121 AGAGAAATCTCTCTGGGTTTCCAGATCTGTAGCAGAGAGATCTGTAGGAGGCTGTCT 180
QY 618 GCTCTGTGGCAATTAAGGATGATCTGTAGGAGAGTGGAGGAGAAACAATCCCTG 677
Db 181 GCTCTGTGGCAATTAAGGATGATCTGTAGGAGAGTGGAGGAGAAACAATCCCTG 239
QY 678 GAAGACTATCAGGGGTTCCCTTTGAC-----CCACAGCAGCCTTGTGGACAGGACTTT 732
Db 240 GAATACTATGATGATGTTCCCTTTGACACACACAGCAGCAGCCTTGTGGAGCTTT 299
QY 733 TCCCTCAGAGCCTTGTCTGTCTGACACTCAATGTGTGTGGGGGTCTGACCTCAGCTC 792
Db 300 TCCCTCAGAGCCTTGTCTGTCTGACACTCAATGTGTGTGGGGGTCTGACCTCAGCTC 359
QY 793 CTCTGAGTCCCTTGGCTCCACTGAGTCAAGTCAAGACCGGAGGTCCCTGCTCCCGCTCAGA 852
```

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|||||
Db 360 TTCTAGAGCCCTCAGCCCTCCAGCTCAGGACAGACAGAGTGGCTGTCCCTC-TTCAGG 418
OY 853 GACTAGAACTTCCAAAGAAATAGAGATTTATCCAGGTGCCCGTGTCCAGCTGTGTCT 912
Db 419 GACTAGAAATTTCCACGGAATAGAGATATATCCAGGTGCTGTGTCCAGCTGTGTCT 478
OY 913 GGGTCTGTGTCTCCCTTCCACCCAGAGATATGTTGATTTCTTAAAGATGTACATCC 972
Db 479 GGGTCTGTGTCTCCCTTCCACCCAGAGTGTCTGTCTTCAAGATAGCCACAT-- 536
OY 973 AGGTCTGTGTGTGTCCATGAGATGCAAGTGTGTGAATTTCTGTCTTCTTCTT 1032
Db 537 GTGTCTGTGTGTGTGTCCATGAGATGCAAGTGTGTGAATTTCTGTCTTCTTCTG 596
OY 1033 TCAG 1036
Db 597 ACAG 600
```

```
RESULT 9
US-09-964-261-398
; Sequence 398, Application US/09964261
; Publication No. US20020197613A1
; GENERAL INFORMATION:
; APPLICANT: De Canck, Ilse
; APPLICANT: Rombout, Annelies
; APPLICANT: Rossau, Rudi
; TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES
; FILE REFERENCE: IGI-002
; CURRENT APPLICATION NUMBER: US/09/964,261
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: EP 99870068.6
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/138,614
; PRIOR FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 398
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-261-398
```

Query Match 17.4%; Score 426; DB 9; Length 600;
Best Local Similarity 86.1%; Pred. No. 1,7e-113;
Matches 520; Conservative 0; Mismatches 75; Indels 9; Gaps 4;

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OY 438 GTACCAAGGGGAGTGGGGGCGCTCCTGATCTCTGTAGACCTTCAGCCTGGCTAGCA 497
Db 1 GTACCAAGGGGAGTGGGGGCGCTCCTGATCTCTGTAGATCTCCGGGCTGGCTCCCA 60
OY 498 CAAGAGAGAGGAGAAATGGGACCAACACTAGAAATATGCGCCCTCCTGTGTCTGAGGG 557
Db 61 CAAGAGAGGAGAGCAATTTGGGACCAACACTAGAAATATGCGCCCTCCTGTGTCTGAGGG 120
OY 558 AGAGAAATCTCTCGGGTTTCCAGATCTGTACAGAGAGTGTGTGGGGGCGGTCT 617
Db 121 AGAGAAATCTCTCGGGTTTCCAGATCTGTACAGAGAGTGTGTGGGGGCGGTCT 180
OY 618 GCTCTGTGACCAATTTAAGGATGAAGTCTCTGAGGAGTGTGAAGGAGAAACATCCCTG 677
Db 181 GCTCTGTGACCAATTTAAGGATGAAGTCTCTGAGGAGTGTGAAGGAGAAACATCCCTG 239
OY 678 GAAGACTGATCAGGGGTTCCCTTTGAC-----CCACAGCAGAGCTTGGCACAGACTTT 732
Db 240 GAATATCTGATGAGTGTGTCTCTTGTGACACACAGAGGAGAGGCTTGGGCGGTGACTTT 299
OY 733 TCCTCTAGAGGCTTGTCTGTCTGCTCAGCTCACTCAATGTGTGGGGGTCTGACTCCAGCTC 792
Db 300 TCCTCTAGAGGCTTGTCTGTCTGCTCAGCTCACTCAATGTGTGGGGGTCTGACTCCAGCAGC 359
OY 793 CTCTGAGTCCCTTGGCTCCACTCAGGTCAAGAACCGGAGGTCCCTGTCTCCCGGCTCAGA 852
```

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|||||
Db 360 TTCTAGAGCCCTCAGCCCTCCAGCTCAGGACAGACAGAGTGGCTGTCCCTC-TTCAGG 418
OY 853 GACTAGAACTTCCAAAGAAATAGAGATTTATCCAGGTGCCCGTGTGTCCAGCTGTGTCT 912
Db 419 GACTAGAAATTTCCACGGAATAGAGATATATCCAGGTGCTGTGTCCAGCTGTGTCT 478
OY 913 GGGTCTGTGTCTCCCTTCCACCCAGAGATATGTTGATTTCTTAAAGATGTACATCC 972
Db 479 GGGTCTGTGTCTCCCTTCCACCCAGAGTGTCTGTCTTCAAGATAGCCACAT-- 536
OY 973 AGGTCTGTGTGTGTCCATGAGATGCAAGTGTGTGAATTTCTGTCTTCTTCTTCTT 1032
Db 537 GTGTCTGTGTGTGTGTCCATGAGATGCAAGTGTGTGAATTTCTGTCTTCTTCTG 596
OY 1033 TCAG 1036
Db 597 ACAG 600
```

```
RESULT 10
US-09-964-261-405
; Sequence 405, Application US/09964261
; Publication No. US20020197613A1
; GENERAL INFORMATION:
; APPLICANT: De Canck, Ilse
; APPLICANT: Rombout, Annelies
; APPLICANT: Rossau, Rudi
; TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES
; FILE REFERENCE: IGI-002
; CURRENT APPLICATION NUMBER: US/09/964,261
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: EP 99870068.6
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/138,614
; PRIOR FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 405
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-261-405
```

Query Match 17.2%; Score 421.2; DB 9; Length 600;
Best Local Similarity 85.6%; Pred. No. 4.1e-112;
Matches 517; Conservative 0; Mismatches 78; Indels 9; Gaps 4;

```
OY 438 GTACCAAGGGGAGTGGGGGCGCTCCTGATCTCTGTAGACCTTCAGCCTGGCTAGCA 497
Db 1 GTACCAAGGGGAGTGGGGGCGCTCCTGATCTCTGTAGATCTCCGGGCTGGCTCCCA 60
OY 498 CAAGAGAGAGGAGAAATGGGACCAACACTAGAAATATGCGCCCTCCTGTGTCTGAGGG 557
Db 61 CAAGAGAGGAGAGCAATTTGGGACCAACACTAGAAATATGCGCCCTCCTGTGTCTGAGGG 120
OY 558 AGAGAAATCTCTCGGGTTTCCAGATCTGTACAGAGAGTGTGTGGGGGCGGTCT 617
Db 121 AGAGAAATCTCTCGGGTTTCCAGATCTGTACAGAGAGTGTGTGGGGGCGGTCT 180
OY 618 GCTCTGTGACCAATTTAAGGATGAAGTCTCTGAGGAGTGTGAAGGAGAAACATCCCTG 677
Db 181 GCTCTGTGACCAATTTAAGGATGAAGTCTCTGAGGAGTGTGAAGGAGAAACATCCCTG 239
OY 678 GAAGACTGATCAGGGGTTCCCTTTGAC-----CCACAGCAGAGCTTGGCACAGAGACTTT 732
Db 240 GAATATCTGATGAGTGTGTCTCTTGTGACACACAGCGGAGAGGCTTGGGCGGTGACTTT 299
OY 733 TCCTCTAGAGGCTTGTCTGTCTGCTCAGCTCACTCAATGTGTGGGGGTCTGACTCCAGCTC 792
Db 300 TCCTCTAGAGGCTTGTCTGTCTGCTCAGCTCACTCAATGTGTGGGGGTCTGACTCCAGCAGC 359
OY 793 CTCTGAGTCCCTTGGCTCCACTCAGGTCAAGAACCGGAGGTCCCTGTCTCCCGGCTCAGA 852
```

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|||||
Db 360 TTCTGAGTCCCTCAGACCCCTCCACTCAGGTCAGACAGCAAGTCGCTGTCCCTC-TCACAG 418
OY 853 GACTAGACTTTTCCAGGAATAGAGATTTATCCAGGTGCCCGTCCAGCTGGGTCT 912
Db 419 GACTAGAAATTTTCCAGGAATAGAGATTTATCCAGGTGCCCGTCCAGCTGGGTCT 478
OY 913 GGGTCTGTGCTCCCTCCCTCCACCCAGAGATCTGTGTTCAATTCATAGATGTACATCC 972
Db 479 GGGTCTGTGCTCCCTCCCTCCACCCAGAGATCTGTGTTCAATTCATAGATGTACATCC 536
OY 973 AGGTCTGTGCTCCCTCCCTCCACCCAGAGATCTGTGTTCAATTCATAGATGTACATCC 1032
Db 537 GTGTCTGTGAGAGGTGTCCCATTTACAGATGCCAATATGCTGAATGTTCAGCTTCCG 596
OY 1033 TCAG 1036
|||
Db 597 ACAG 600

```

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RESULT 11
US-09-964-261-406
; Sequence 406, Application US/09964261
; Publication No. US20020197613A1
; GENERAL INFORMATION:
; APPLICANT: De Canck, Ilse
; APPLICANT: Rombout, Annelies
; APPLICANT: Rossau, Rudi
; TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES
; FILE REFERENCE: IGJ-002
; CURRENT APPLICATION NUMBER: US/09/964,261
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: EP 99870068.6
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/138,614
; PRIOR FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 406
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-261-406

```

```

Query Match 17.2%; Score 421.2; DB 9; Length 600;
Best Local Similarity 85.6%; Pred. No. 4.1e-112;
Matches 517; Conservative 0; Mismatches 78; Indels 9; Gaps 4;

```

```

OY 438 GTACCAGGGGAGTGGGGGCTCCCTGATCTCCTGTAGACCTCTCAGCCTGGCCTAGCA 497
Db 1 GTACCAGGGGAGTGGGGGCTCCCTGATCTCCTGTAGACCTCTCAGCCTGGCCTAGCA 60
OY 498 CAAGGAGAGGAGAAATGGGACCAACACTAGATATCGCCCTCCCTGTGCTCTGAGGG 557
Db 61 CAAGGAGAGGAGAAATGGGACCAACACTAGATATCGCCCTCCCTGTGCTCTGAGGG 120
OY 558 AGAGGATCTCTGCTGGGCTTCCAGATCTCTGACAGAGATGATCTGAGGGCCCTCT 617
Db 121 AGAGGATCTCTGCTGGGCTTCCAGATCTCTGACAGAGATGATCTGAGGGCCCTCT 180
OY 618 GCTCTCTGGGCAATTAAGGATGAAGTCTCTGAGGAGTGGAGGAGAGCAATCCCTG 677
Db 181 GCTCTCTGGGCAATTAAGGATGAAGTCTCTGAGGAGTGGAGGAGAGCAATCCCTG 239
OY 678 GAAGACTGATCAGGGGCTTCCCTTGAC-----CCACAGAGAGCTTGGCACAGGACTTT 732
Db 240 GAATGATGATGAGGTTCCTTTGACACACACCGGAGAGAGCTTGGGCCCTGACTTT 299
OY 733 TCCTCTCAGGCTTGTCTCTGCTCCTCAGACTCAATGTGTGGGGGTCTGATCCAGCTC 792
Db 300 TCCTCTCAGGCTTGTCTCTGCTCCTCAGACTCAATGTGTGGGGGTCTGATCCAGCTC 359
OY 793 CTCGTAGTCCCTTGGCTCCACTCAGAGTCAAGAACGGAGAGTCCCTGTCCGCCCTCAGA 852

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|||||
Db 360 TTCTGAGTCCCTCAGACCCCTCCACTCAGTCCAGACAGCAAGTCCCTGTCCCTC-TCACAG 418
OY 853 GACTAGAACTTTTCCAGGAATAGAGATTTATCCAGGTGCCCGTCCAGCTGGGTCT 912
Db 419 GACTAGAAATTTTCCAGGAATAGAGATTTATCCAGGTGCCCGTCCAGCTGGGTCT 478
OY 913 GGGTCTGTGCTCCCTCCCTCCACCCAGAGATCTGTGTTCAATTCATAGATGTACATCC 972
Db 479 GGGTCTGTGCTCCCTCCCTCCACCCAGAGATCTGTGTTCAATTCATAGATGTACATCC 536
OY 973 AGGTCTGTGCTCCCTCCCTCCACCCAGAGATCTGTGTTCAATTCATAGATGTACATCC 1032
Db 537 GTGTCTGTGAGAGGTGTCCCATTTACAGATGCCAATATGCTGAATGTTCAGCTTCCG 596
OY 1033 TCAG 1036
|||
Db 597 ACAG 600

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```

RESULT 12
US-09-964-261-399
; Sequence 399, Application US/09964261
; Publication No. US20020197613A1
; GENERAL INFORMATION:
; APPLICANT: De Canck, Ilse
; APPLICANT: Rombout, Annelies
; APPLICANT: Rossau, Rudi
; TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES
; FILE REFERENCE: IGJ-002
; CURRENT APPLICATION NUMBER: US/09/964,261
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: EP 99870068.6
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/138,614
; PRIOR FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 399
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-261-399

```

```

Query Match 16.8%; Score 410.8; DB 9; Length 599;
Best Local Similarity 85.6%; Pred. No. 4.2e-109;
Matches 517; Conservative 0; Mismatches 77; Indels 10; Gaps 5;

```

```

OY 438 GTACCAGGGGAGTGGGGGCTCCCTGATCTCCTGTAGACCTCTCAGCCTGGCCTAGCA 497
Db 1 GTACCAGGGGAGTGGGGGCTCCCTGATCTCCTGTAGACCTCTCAGCCTGGCCTAGCA 60
OY 498 CAAGGAGAGGAGAAATGGGACCAACACTAGATATCGCCCTCCCTGTGCTCTGAGGG 557
Db 61 CAAGGAGAGGAGAAATGGGACCAACACTAGATATCGCCCTCCCTGTGCTCTGAGGG 120
OY 558 AGAGGATCTCTGCTGGGCTTCCAGATCTCTGACAGAGATGATCTGAGGGCCCTCT 617
Db 121 AGAGGATCTCTGCTGGGCTTCCAGATCTCTGACAGAGATGATCTGAGGGCCCTCT 180
OY 618 GCTCTCTGGGCAATTAAGGATGAAGTCTCTGAGGAGTGGAGGAGAGCAATCCCTG 677
Db 181 GCTCTCTGGGCAATTAAGGATGAAGTCTCTGAGGAGTGGAGGAGAGCAATCCCTG 239
OY 678 GAAGACTGATCAGGGGCTTCCCTTGAC-----CCACAGAGAGCTTGGCACAGGACTTT 732
Db 240 GAATGATGATGAGGTTCCTTTGACACACACCGGAGAGAGCTTGGGCCCTGACTTT 299
OY 733 TCCTCTCAGGCTTGTCTCTGCTCCTCAGACTCAATGTGTGGGGGTCTGATCCAGCTC 792
Db 300 TCCTCTCAGGCTTGTCTCTGCTCCTCAGACTCAATGTGTGGGGGTCTGATCCAGCTC 359
OY 793 CTCGTAGTCCCTTGGCTCCACTCAGAGTCAAGAACGGAGAGTCCCTGTCCGCCCTCAGA 852

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Db 360 TTCTGAGTCCCTCAGCTCCAGCTAGGTGAGGACAGAGTGGTGTCCCTC-TTCAGG 418
QY 853 GACTAGAACTTCCAGGAATAGAGATTAATCCAGGTGCCGTGTCAGGCTGGTCT 912
Db 419 GACTAGAA-TTCCACGGAATAGAGATTAATCCAGGTCGTGTCAGGCTGGTCT 477
QY 913 GGGTTCGTGCTCCCTTCCACCCAGGATCTGTGTTCAATCTTAGAGATGTCACATCC 972
Db 478 GGGTTCGTGCTCCCTTCCACCCAGGATCTGTGTTCAATCTTAGAGATGTCACATCC 535
QY 973 AGGTGCTGCTGAGGTCGTCAGATGAGATGCAAGTCTGTAATTTCTGACTTCTCTT 1032
Db 536 GTGTGCTGAGGAGTGTCCATGACAGATACCCCAATGCTGTATGTTCTGACTTCTCTG 595
QY 1033 TCAG 1036
Db 596 TCAG 599
|||||
RESULT 13
US-09-864-761-4806/c
: Sequence 4806, Application US/09864761
: Patent NO. US20020048763A1
: GENERAL INFORMATION:
: APPLICANT: Penn, Sharon G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
: FILE REFERENCE: Aecomica-X-1
: CURRENT APPLICATION NUMBER: US/09/864,761
: CURRENT FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 2000-02-04
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 2000-08-03
: PRIOR APPLICATION NUMBER: GB 24263,6
: PRIOR FILING DATE: 2000-10-04
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: PCT/US01/00666
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00667
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00664
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00669
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00665
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00668
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00663
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00662
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00661
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00670
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 2000-09-21
: PRIOR APPLICATION NUMBER: US 09/608,408
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: US 09/774,203
: PRIOR FILING DATE: 2001-01-29
: NUMBER OF SEQ ID NOS: 49117
: SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
: SEQ ID NO 4806
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: LENGTH: 412
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO AF055066.1
: OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 11
: OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 38
: OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 33
: OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 25
: OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 16
: OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.4
: OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 7.5
: OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 59
: OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 25
: OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 13
US-09-864-761-4806
Query Match 16.7%; Score 408.8; DB 10; Length 412;
Best Local Similarity 99.5%; Pred. No. 1.3e-108;
Matches 410; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1135 ACCTGCGAGCGGGATGGGAGGAGACACAGACCAGAGCTGAGCTGTGAGACAGGCTT 1194
Db 352 ACCTGCGAGCGGGATGGGAGGAGACACAGACCAGAGCTGAGCTGTGAGACAGGCTT 293
QY 1195 GCAGGGGATGAACCTTCCAGAAAGTGCGAGCTGTGTGCTTCTGTGAGAGACAG 1254
Db 292 GCAGGGGATGAACCTTCCAGAAAGTGCGAGCTGTGTGCTTCTGTGAGAGAGAG 233
QY 1255 AGATACACGTGCTATGTGACATGAGGCTCCGAGGCCCTCATGCGAGATGAGAT 1314
Db 232 AGATACACGTGCTATGTGACATGAGGCTCCGAGGCCCTCATGCGAGATGAGAT 173
QY 1315 AAGGAGGAGATGAGGAGCATCATGCTGTAGGAGAAAGCAGAGCCTCTCTGAACCTT 1374
Db 172 AAGGAGGAGATGAGGAGCATCATGCTGTAGGAGAAAGCAGAGCCTCTCTGAACCTT 113
QY 1375 TAACAGGGGTGGTGTGAGGCTGGGGCTGAGAGACCTTACCTTCTTTCCAG 1434
Db 112 TAACAGGGGTGGTGTGAGGCTGGGGCTGAGAGACCTTACCTTCTTTCCAG 53
QY 1435 AGCAGTCTTCCCTGCCACCATCCCATCATGGGTATGCTGGGCTGGGT 1486
Db 52 AGCAGTCTTCCCTGCCACCATCCCATCATGGGTATGCTGGGCTGGGT 1
RESULT 14
US-09-964-261-444
: Sequence 444, Application US/09964261
: Publication No. US20020197613A1
: GENERAL INFORMATION:
: APPLICANT: De Canck, Ilse
: APPLICANT: Rombout, Annelies
: APPLICANT: Rossau, Rudi
: TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES
: FILE REFERENCE: IGJ-002
: CURRENT APPLICATION NUMBER: US/09/964,261
: PRIOR FILING DATE: 2001-09-25
: PRIOR APPLICATION NUMBER: EP 99870068.6
: PRIOR FILING DATE: 1999-04-09
: PRIOR APPLICATION NUMBER: US 60/138,614
: PRIOR FILING DATE: 1999-06-11
: NUMBER OF SEQ ID NOS: 446
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 444
: LENGTH: 598
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-964-261-444
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Query Match 16.7%; Score 406.8; DB 9; Length 598;
Best Local Similarity 86.3%; Pred. No. 6,1e-108;
Matches 521; Conservative 0; Mismatches 72; Indels 11; Gaps 6;

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QY 438 GTACAGGGGCGAGTGGGGGCGCTCCCTGATCTCTGTAGACCTCTGACGCTTGCCCTAGCA 497
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Db 1 GTACACAGGGGCGACAGGGGCGCTCCCTGATCTCTGTAGATCTCTGCGGGCTGCGCTCCCA 60
QY 498 CAAGGAGAGGAGGAAATGGGACCAACATAGATATCCGCCCTCCCTCTGCTCTGAGGG 557
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Db 61 CAAGGAGGAGAGACAAATTTGGACCAACACTAGATATCGCCCTCCCTGCTCTGAGGG 120
QY 558 AGAGGAATCTCTCTGGGTTTCCAGATCTCTGTACAGAGATGATTTCTGAGGGCCGCTCT 617
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Db 121 AGAGGAATCTCTCTGGGTTTCCAGATCTCTGTACAGAGATGATTTCTGAGGTTCCGCT 180
QY 618 GCTCTCTGGGACAAATTAAGGATGAAGTCTCTGAGGAGTGGAGGGAAGACAAATCCCTG 677
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Db 181 GCTCTCTGACAAATTAAGGATGAAGTCTCTGAGGAAAT-GACGGGAAGACGATCCCTG 239
QY 678 GAAGACTGATCAGGGGTTCCCTTGAC-----CCACAGACGCTTGACACGACGCTTT 732
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QY 793 CTCTGAGTCCCTTGCGCTCAGCTCAGAGTCAAGACCGGAGTCCCTGCTCCCGCTCAGA 852
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Db 360 TTCTGAGTCCCTTGCGCTCAGCTCAGAGTCAAGAGTGGCTGCTCCTC-TTCAGG 418
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Db 419 GACTAGAAATTTTCCAGAGATAGAGATTAATCCAGGTCCCTGCTCAGGCTGGGTCT 478
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Db 479 GGGTTTGTGCTCCCTTCCCAACCCAGGTATCTGGTTCAATCTTAGATGTGCAATCC 536
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RESULT 15

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US-09-964-261-402
; Sequence 402, Application US/09964261
; Publication No. US20020197613A1
; GENERAL INFORMATION:
; APPLICANT: De Canck, Ilse
; APPLICANT: Rombout, Annelies
; APPLICANT: Rossau, Rudi
; TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES
; FILE REFERENCE: IGJ-002
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,261
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/138,614
; PRIOR FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 402
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-261-402
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Query Match 16.5%; Score 402.4; DB 9; Length 579;
Best Local Similarity 84.5%; Pred. No. 1,1e-106;
Matches 507; Conservative 0; Mismatches 71; Indels 22; Gaps 4;

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QY 438 GTACAGGGGCGAGTGGGGGCGCTCCCTGATCTCTGTAGACCTCTGACGCTTGCCCTAGCA 497
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Db 1 GTACACAGGGGCGACAGGGGCGCTCCCTGATCTCTGTAGATCTCTGCGGGCTGCGCTCCCA 60
QY 498 CAAGGAGAGGAGGAAATGGGACCAACATAGATATCCGCCCTCCCTCTGCTCTGAGGG 557
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Db 61 CAAGGAGGAGAGACAAATTTGGACCAACACTAGATATCGCCCTCCCTGCTCTGAGGG 120
QY 558 AGAGGAATCTCTCTGGGTTTCCAGATCTCTGTACAGAGATGATTTCTGAGGGCCGCTCT 617
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 121 AGAGGAATCTCTCTGGGTTTCCAGATCTCTGTACAGAGATGATTTCTGAGGTTCCGCT 180
QY 618 GCTCTCTGGGACAAATTAAGGATGAAGTCTCTGAGGAGTGGAGGGAAGACAAATCCCTG 677
    ||||||| ||||||| ||||||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 GCTCTCTGACAAATTAAGGATGAAGTCTCTGAGGAAAT-GACGGGAAGACGATCCCTG 239
QY 678 GAAGACTGATCAGGGGTTCCCTTGAC-CCACAGACGCTTGACACGACGCTTTTCC 736
    ||| ||||| ||| ||||||| ||| ||| ||||||| ||| ||||||| ||| |||||
Db 240 GAATACTGATGATGTTTCCCTTTGACACACCGGACGAGCTTGAGGCGCGTACTTTCT 299
QY 737 TCCCTCAGGCGCTTGTCTCTGCTCACAACCTCAATGTGTGGGGGCTGACCTCAGCTCT 796
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Db 300 CTGAGGCGCTTGTCTCTGCTCACAACCTCAATGTGTGGGGGCTGAGTCCAGCACTTCT 359
QY 797 GAGTCCCTTGCGCTCAGCTCAGAGTCAAGACCGGAGTCCCTGCTCCCGCTCAGAGACT 856
    ||||| ||| ||||||| ||||||| ||| ||| ||| ||| ||| ||| |||
Db 360 GAGTCTCAGCGCTCAGCTCAGAGTCAAGAGTCAAGAGTGGCTGCTCCT----- 405
QY 857 AGAATTTCCAGAGATAGAGATTAATCCAGGTCCCGGTGCGAGGCTGGTGTCTGGGT 916
    ||| ||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 406 ---CTTCTCAGGGAATAGAGATTAATCCAGGTCCCGGTGCTCAGGCTGGTGTCTGGGT 461
QY 917 TCTGCTCCCTTCCCAACCCAGGTATCTGGTTCAATCTTAGATGTGCAATCCAGGT 976
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Db 462 TCTGTGCTCTTCTCCCATTCGCCGGGTGCTGCTCATTTCTCAGATGTGCCACATGC--GT 519
QY 977 GCTGCTGAGTGTCCCATGAGAGATGAAGTCTGAATTTCTGACTCTTCTCTCAG 1036
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Db 520 GCTGAGAGAGTGTCCCATGAGAGATGAAGTCTGAATTTCTGACTCTTCTCTCAG 579
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Search completed: January 31, 2003, 02:21:31
Job time : 175 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 22:01:58 ; Search time 3060 Seconds
(without alignments)
12924.634 Million cell updates/sec

Title: US-09-622-846-16
Perfect score: 2442
Sequence: 1 tactcccgagctcgcgggtc.....tgcctatgccttccttg 2442

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809774376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: em_estba:*
2: em_estlum:*
3: em_estlin:*
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6: em_estlpl:*
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8: em_hlc:*
9: gp_estl1:*
10: gp_estl2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_dln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	548.2	22.4	963	13	BM475710	BM475710 AGENCOURT
2	481.8	19.7	1042	12	BF797314	BF797314 602256935
3	476	19.5	676	10	AV730970	AV730970 AV730970
4	474	19.4	673	12	BF739367	BF739367 PM0-KT004
5	467	19.1	698	10	AV730652	AV730652 AV730652
6	450.8	18.5	637	9	AL602989	AL602989 DXFZP086J

7	443.6	18.2	953	9	AL538335	AL538335
8	437	17.9	950	14	BO711975	BO711975 AGENCOURT
9	435.2	17.8	992	14	BO710264	BO710264 AGENCOURT
10	405.6	16.6	732	10	AV695124	AV695124
11	398.8	16.3	655	17	AG094772	AG094772 Pan t1091
12	395.2	16.2	713	17	AG119067	AG119067 Pan t1091
13	394.2	16.1	742	10	AV694018	AV694018
14	385	15.8	1027	9	AL567261	AL567261
15	382.4	15.7	731	12	BS548958	BS548958 602575796
16	382.2	15.7	1018	17	AF057114	AF057114 AF057114
17	371	15.2	822	9	AL519039	AL519039
18	350.4	14.3	463	12	BF873745	BF873745
19	350.4	14.3	674	14	BO328156	BO328156 MR4-RT004
20	349	14.3	467	14	BM694948	BM694948 UI-E-C11-
21	345.6	14.2	605	14	BO328128	BO328128 MR4-RT004
22	338.6	13.9	499	12	BF871243	BF871243
23	336	13.8	450	10	AM819527	AM819527 RC5-ST029
24	320.4	13.1	479	10	AM847815	AM847815 IL3-CT021
25	319.4	13.1	536	10	AM603938	AM603938 IL3-CT021
26	319.4	13.1	663	17	AC039086	AC039086 Pan t1091
27	312.4	12.7	382	13	BI031182	BI031182 IL5-MT026
28	309.4	12.7	574	14	W60762	W60762 zd26c08.r1
29	308.4	12.6	1032	14	BO706569	BO706569 AGENCOURT
30	306.6	12.5	472	12	BF902064	BF902064 PM1-MT020
31	305.2	12.5	555	12	BF953853	BF953853 MR0-NN117
32	299.8	12.3	1101	12	BE869028	BE869028 601444936
33	295.2	12.1	918	9	AL542545	AL542545
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35	291.6	11.9	512	14	BO328194	BO328194 MR4-RT004
36	291.2	11.9	617	10	AM206422	AM206422 UI-H-B11-
37	288.8	11.8	719	14	BO016844	BO016844 UI-H-D10-
38	283.8	11.6	429	10	AV696063	AV696063 AV696063
39	282.4	11.6	487	14	BO300975	BO300975 PM0-KT004
40	281	11.5	491	10	AV732289	AV732289 AV732289
41	277.2	11.4	431	10	BE165654	BE165654 CM4-HT048
42	276.8	11.3	845	9	AL542095	AL542095
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ALIGNMENTS

RESULT 1
LOCUS BM475710 963 bp mRNA linear EST 05-FEB-2002
DEFINITION AGENCOURT_6480189 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5575764
5', mRNA sequence.
ACCESSION BM475710
VERSION BM475710.1 GI:18524752
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 963)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Plate: LLM12326 row: 1 column: 13
High quality sequence stop: 716.
Location/Qualifiers
1. 963

FEATURES
source

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/organism="Homo sapiens"
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/clone_image="5575764"
/clone_id="NIH_MGC_92"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pCMVSPORT6; Site_1: NotI.
Site_2: SalI; Cloned unidirectionally; 0.190-ct primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies
Note: this is a NIH_MGC library."

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Db	3	ATGATTTGGCTGGACCTGGGGTTCGACGAGCCCTCTCCGGGGTATGAACATATGCC	62		
OY	242	TACATGGCAAGATTACCTGCGCTGGAACGAGGACCTGCGCTCTGACCGACGAGGAC	301		
Db	63	AAGATGGCAAGATTACATATGCGCGGAACCTAGGACCTGCGCTCTGACCGCGGCGAC	122		
OY	302	ACTGCGGCTCAGATCTTCCAAAGCGCAAGTGTAGGCGGCCAATGTGCTGAACAAAGAGA	361		
Db	123	ATGCGGGCTCAGATCACCAAGCGCAAGTGTAGGCGGCCAAGATTGTGAGGACAGATCAG	182		
OY	362	GCCCTACCTGGAGGCGACGTGCGTGGAGTGGCTCCACATATACCTGGAGAACGGGAAGAG	421		
Db	183	GCTTACTGGAGGCGACGTGCGTGGAGAGGCT - CGCAGACACTGGAGAACGGGAAGAG	241		
OY	422	ATGCTGAGGCGCGGGTACCAAGGGGCACTGAGGGGCGCTCCCTATCTCCTGTAGACTTC	481		
Db	242	ACGCTGAGCTCAAGGGTACCAAGGAAACACAGACGCTCCCTATCTCCTGTAGACTTC	301		
OY	482	TCACCCCTGGCTCAGCAAGAGAGAGGAAATGGGACCAACACTAGAAATATGCGCTTC	541		
Db	302	CTGGGCTGGCTTCCCAAGAGAGAGAAATGGGACCAACACTAGAAATATGCTCTTC	361		
OY	542	CCCTGGGCTGGAGGAGAGAAATCCTCGGGTTCCAGATCCTGTATCCAGAGAGATGAT	601		
Db	362	TCCTGGGCTGGAGGAGAGAAATCCTCGGGTTCCAGATCCTGTATCCAGAGAGATGAT	421		
OY	602	TCTTGGGCGCGCTCTGCTCTCTGGGACAAATTAAGGATGAAGTCTCTGAGGAGTGGAG	661		
Db	422	TCTTGGGCGCTCTGCTCTCTGGGACAAATTAAGGATGAAGTCTCTGAGGAGTGGAG	480		
OY	662	GGGAGAGCAATCCCTGGAGAGCATGATCAGGGGTTCCCTTACACCCG - CAGAGCGCT - G	719		
Db	481	GGGAGAGCAATCCCTGGAGATCTGATGAGGGTTCCTCTTATCACACGACAGACCTCTGG	540		
OY	720	GCACCAAGCAATTTCCCTCAGGCGCTTGTCTCTGCTCCTCACACTCAATGTGTGTGGGGT	779		
Db	541	GCACCGCTTACTTTCCCTCAGGCGCTTGTCTCTCTTACACTCAATGTGTGTGGGGT	600		
OY	780	CTGACCTCCACTCTCTGAGTCCCTTGGGCTCAGTCAAGTCAACACGGAGGCGCTGC	839		
Db	601	CTGAGTCCACTCTTCTGAGTCCCTCAGGCTCAGTCAAGTCAAGGACCAAGTCACTGT	660		
OY	840	TCCCGCGCTCAGAGACTAGAACTTCCAAAGAA - TAGAGATTAATCCAGGTGCCGCTG	898		
Db	661	TCCCTC - CTCAGGAGCAATTTCCAAAGAAATTCGAGATTAATCCAGATACCTGTG	719		
OY	899	CCAGGCTGGT - GTCGTGGTCTGTGCTCCCTTCCACACCCAGGAT - CTGGTCAATTC	956		
Db	720	CCAGGTTGGTGTGTGGTCTGTGTCCCTTCCACACCCAGGATGTCCTGTCAATTC	779		
OY	957	TAGATGTGCATCAAGGTGCTGCTGAGTGTCCCATGAGAGATGCAAGATGCTTGAAAT	1016		
Db	780	CAGATGTGCATCAAGT - GTGCTGTGGAGGCTGTCAATGAGAGATGCAAGATGCTTGAA	838		

QY	1017	TTTTCT	1021
Db	839	TTTTTT	843

RESULT 2	BF797314	1042 bp	mRNA	linear	EST: 12-JAN-2001
LOCUS	60222695	NT_H_MGC_85	Homo sapiens	cdna	clone IMAGE:434036 5,
DEFINITION	mRNA sequence.				
ACCESSION	BF797314				
VERSION	BF797314.1	GI:12102368			

REFERENCE	1 (bases 1 to 1042)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Louis Staudt, M.D., Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: L1AM952 row: e column: 09
 High quality sequence stop: 703.

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Location/Qualifiers
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/lab_host="DH10b (phage-resistant)"
/note="Organ: lymph; Vector: PCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally: oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies
Note: this is a NIH_MGC library."

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BASE COUNT	252 a	285 c	306 g	199 t
ORIGIN				
Query Match	19.7%	Score 481.8;	DB 12;	Length 1042;
Best Local Similarity	83.9%	Pred. No. 8.2e-114;		
Matches 627; Conservative	0;	Mismatches 112;	Indels 8;	Gaps 7

Q7 230 ACCGACGGAGCACACTGGCGCTCAGATCTCCAAAGGCCAAGTGTGAAGGGGCCCATGTGCCT 349
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D8 1 ACCCGCGGAGCATGGGCGGTCAATACCAACAAGCCCAAGTCGGAGCGCAAGAATTTCGA 60

Dc	GAGCAGATCAAGGCGCTACCTGGAGGGCCAGTCTGTGGAGAAGCTT - CGCAGACACTTGGA 119
Dy	AACCGGAGSAGATTCGTCGACGCAGCGCGGGTACCAAGGGCACTGTGGGCGCGCTGCCCTCATCTC 469

Db 120 AACGGGAAGAGACGCTGCACGCTCACAGGGTACCAGGGACCAAGACGCTCCCTGATGG 179

Qy 470 CCTGTAGACCTCTCAGCGCTGGCCCTAGCACAAGGAGAGAGAGAAAATGGACCAACATG 529

[illegible]

[illegible]

Query Match	19.58;	Score 476;	DB 10;	Length 676;
Best Local Similarity	86.68;	Pred. No. 2.2e-112;		
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QY	1026	CTTCCTTTTGAAGACCCCGGACAGACACAGTGAACCCACACCTCTGTTTGAATATAGAGC	1085
Db	643	CTCCCTCTTCAAGAGCCCGCCAAAGACACAGTGAATCTACACCCCATCTCTGACATATAGGC	584
QY	1086	CACCTTAGGTGCTGGGCGCTTGCTTACCTTCGAGATCATACTAGCTGGACGG	1145
Db	583	CACCTTAGGTGCTGGGCGCTTGCTTACCTTCGAGATCATACTAGCTGGACGG	524
QY	1146	GCATGGGAGAGACACAGACAGTGAAGTGTGGAGACAGGCTTCAGAGGATG	1205
Db	523	GCATGGGAGAGACAGACAGTGAAGTGTGGAGACAGGCTTCAGAGGATG	464
QY	1206	AACCTTCAGAAAGTGGGACAGCTGTGTGTGTGCTTCTTGGAGAGAGATACACGTG	1265
Db	463	AACCTTCAGAAAGTGGGACAGCTGTGTGTGTGCTTCTTGGAGAGAGATACACGTG	404
QY	1266	CCATGTGCAGCATGAGAGGCGCTCCGAGAGCCCTCATGTGATGATGAGAGGAGGA	1325
Db	403	CCATGTGCAGCATGAGAGGCGCTCCGAGAGCCCTCATGTGATGATGAGAGGAGGA	344
QY	1326	TGG- -AGCATCATGTCTTGTAGGAAAGACAGAGCCCTCTGAAAGCCTTTAAAGGGT	1383
Db	343	TGGAGGATCATGTCTTGTCTTTCAGGAAAGAGGAGCCCTTGTGAGAGCCCTCCGAGGGT	284
QY	1384	CGGTGTGAGAGGCTGGGGGTCAGAGAGCCCTCAGCTTCACCTCTTCTCCAGAGCACTTT	1443
Db	283	CAGGGCTGAGAGGCTGGGGGTCAGAGAGCCCTCAGCTTCACCTCTTCTCCAGAGCACTTT	227
QY	1444	CCCTGCCACCAATCCCATCATGAGGATGCTGTGGGCGCTGTTGCTTCGACAGCTGTG	1503
Db	226	CCAGCCACCAATCCCATCATGAGGATGCTGTGGGCGCTGTTGCTTCGACAGCTGTG	167
QY	1504	TCACGTAGAGCTGGGTCGCTGCTGTGCTGTGTGAGAAAGAGAGCTCAGTTAAGGAAGG	1563
Db	166	TCCTGTGAGCTGTGGTGTGCTGTGTGATATGAGAGGAAGAGCTCAGGTGGGAA- GGG	108
QY	1564	TGACAAATGGGGCTGAGTTTCTGTGCCACATGGGGGTTTCAAGCCCGAGTGAAGAAGT	1623
Db	107	AGAAGGTGGGGCTGAGTTTCTGTGCCACATGGGGGTTTCAAGCCCGAGTGAAGAAGT	48
QY	1624	TGCCCTGCTGTGTACTGGGAAGACACATCCACACTCATGTGGGCTTAC	1670
Db	47	TGTCCTGCTGTGTACTGGGAAGACACATCCACACACGAGGCTTAC	1
RESULT 4	BF739367/c	673 bp	mRNA linear EST 10-JAN-2001
LOCUS	BF739367		
DEFINITION	PMO-RKD0046-281200-001-f06 KTD046 Homo sapiens cDNA, mRNA sequence.		
ACCESSION	BF739367		
VERSION	BF739367.1	GI:12066043	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
	1 (bases 1 to 673)		
	Nagai,M.A.E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,		
	Desai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,		
	Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,		
	Brumstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare		
	,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and		
	Simpson,A.J.		
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed		
	sequence tags		
JOURNAL	PROC. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)		
MEDLINE	20202663		
COMMENT	Contact: Simpson A.J.G.		

RESULT 6	AL602989	637 bp	mRNA	linear	EST 14-AUG-2001				
LOCUS	AL602989								
DEFINITION	DKEF2686C61220.F1 686 (synonym: h1cc3) Homo sapiens cDNA clone								
ACCESSION	DKEF2686C61220.5	mRNA sequence.							
VERSION	AL602989								
KEYWORDS	AL602989.1	GI:1516495							
SOURCE	EST.								
ORGANISM	human.								
REFERENCE	Homo sapiens								
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
JOURNAL	1 (bases 1 to 637)								
COMMENT	Wambutt, R., Heubner, D., Mewes, W., Well, B. and Wilemann, S.								
	EST (Wambutt, R., Heubner, D., Mewes, H.W., Well, B. and Wilemann, S.)								
	Unpublished (1999)								
	Contact: Wambutt R								

FEATURES
source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DRZP686J1220"
/clone_lib="686 (synonym: hlec3)"
/tissue_type="human skeletal muscle"
/dev_stage="adult"
/lab_host="DH10B"
/notes="vector: pRiplex2; site_1: sfria; site_2: sf1b; dna_collection"
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BASE COUNT	130 a	150 c	170 g	147 t
ORIGIN				
Query Match		18.5%;	Score 450.8;	DB 9;
Best Local Similarity		85.0%;	Pred. No. 7.4e-106;	Length 637

Matches 559; Conservative 0; Mismatches 77; Indels 22; Gaps 4.

Qy	392	CTCCACAGTACTCTTGAAACGGGAGAGAAATCTCTACAGCGCGGGGTACACAGGGGCGAGT	451
Db	1	CTCCGCAAGTACTCTGGAACAGGGGAGAGACGCTGTGAGCGACGGGTACAGGGGGCAC	60
Qy	452	GGGGGGCTCCCTGATCTCTCTGTGAGACCTCTCAAGCTGGGCTTAGCACAAGGAGAGAGGA	511
Db	61	GGGGGGCTTACTGTATGCTGCTGATAGGTCTCCGGGGCTGGGCTTCCCAACAAGAGGGGAAC	120
Qy	512	AAATGGGACCAACATAGAAATATGCGCCCTCCCTGTGCTCTGAGGAGAGGAATCTCTCT	571
Db	121	AAATGGGACCAACACTAGATATATGCGCCCTCCCTGTGCTCTGAGGAGAGGAATCTCTCT	180
Qy	572	GGGTTTCCAGATCCGTACACAGAGATGATTCTGAGGGCCCGGCTCGATCTGGGACAA	631
Db	181	GGGTTTCCAGATCTGTATCCAGAGGTACTCTGAGTTTCCGCGCTGTCTGTACACAA	240
Qy	632	TTTAGGAGATGAATCTCTGAGGAGGTGAGGGGAGAACAAATCCCTGGAGACTGATCAG	691
Db	241	TTTAGGAGATGAATCTCTGTACGGAAT -GACGGAAGAGCATTCCTCGAATACTGATGACT	299
Qy	692	GGTTCCCTTTGAC -CCACAGGAGCCTTGGACACAGACATTTTCCCTGAGGCGCTTGTTC	750
Db	300	GGTTCCCTTTGACCCGCGACGACGACTTTGGAGCCGTATCTTTCTCTCAGGCGCTTGTTC	359
Qy	751	TTGTGCTTCACACTCAATGTGTGTGGGGGTCTGACTCAGACTCCTCTGATCCCTTG6CCT	810
Db	360	TTGTGCTTCACACTCAATGTGTGTGGGGGTCTGACTCAGACTCCTCTGATCCCTTG6CCT	419
Qy	811	CCACTGAGGTCAAGACCGGAGGTGCTCTCCCGGCTCAGAGACTTAGAATTTCCAAAG	870
Db	420	CCACTGAGGTCAAGACCAAGATGCTCTGTCC-----CTCTCTAGGG	461
Qy	871	AAATGAGATTTATCCAGGTGCCCTGTGCCAGGCTGGTGTCTGGGTTCTGTGCTCCCTTC	930
Db	462	AAATGAGATTTATCCAGGTGCCCTGTGCCAGGCTGGGTTCTGTGTCTCTCTTC	521
Qy	931	CCGACCCAGGATATCTGGTTCAATCTTGAAGATGGTCAACATCAGGTGCTCTGAGGTGTC	990
Db	522	CCGATCCCGGGTCTCTGTCTCATTTCTCAAGATGGCCATCATCA--TCTGATGAGTGTGTC	579
Qy	991	CCATGAGAGATGCAAGAGTCTTGAAATTTTCTGACACTCTTCTTGAAGCCGCCCAAGA	1048
Db	580	CCATGAGAGATGCAAAATGCTGTGAATTTTCTGACTCTTCCGCTAGAGCCGCCCAAGA	637

RESULT 7	AL538335	953 bp	mRNA	linear	EST 13-FEB-2001
LOCUS	AL538335				
DEFINITION	AL538335 LTR-Ft013-Fbrn1 Homo sapiens CDNA clone CS0DF02Y1A18 5 prime, mRNA sequence.				

ACCESSION	AL538335
VERSION	AL538335.1
GI	GI:12801828

KEYWORDS	EST.
SOURCE	human
DESCRIPTORS	11070

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 953)
 AUTHORS Li, W.-B., Gruber, C., Jesse, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: genoscope

Genoscope - Centre National de Séquençage
BP 191 91006 Evry cedex - France
Email: segreff@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
SOURCE

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DF027YA18"
/clone_lib="LTI_FL013_FBrn1"

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/dev_stage="pooled tissue from post conception fetuses (20
week, 24 week and 26 week)"
/lab_host="DH10B"
/Note="Organ: Petal brain; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT      191 a      262 c      301 g      198 t      1 others
ORIGIN

Query Match      18.2%; Score 443.6; DB 9; Length 953;
Best Local Similarity 75.3%; Pred. No. 6.4e-104;
Matches 706; Conservative 1; Mismatches 95; Indels 136; Gaps 7;

QY 1034 CAGACCCCCCAGACACAGCTGACCCACCTCTTTGACTATGAGGCCACCTTA 1093
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 147 CGAGCGCCCCAAGACGATATGATCACCGCTCTCTGACCAWAGGCCACCTTA 206
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1094 GGTGCTGGGCGCTGGGCTTACCTGCGAGATCATACTGACCTGCGAGCGGATGGG 1153
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 207 GGTGCTGGGCGCTGGGCTTACCTGCGAGATCATACTGACCTGCGAGCGGATGGG 266
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1154 AGACACGACCCAGACAGCTGAGTGTGAGACGAGCCCTGAGGGATGAACTTTC 1213
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 267 AGACACGACCCAGACAGCTGAGTGTGAGACGAGCCCTGAGGGATGAACTTTC 326
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1214 AGAGTGGGAGAGCTGTGTGCTCTCTGAGAGAGAGAGATACAGCTGATGTC 1273
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 327 AGAGTGGGAGAGCTGTGTGCTCTCTGAGAGAGAGAGATACAGCTGATGTC 386
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1274 AGCATGAGGGGCTGCCGAGACCCCTCATGCTGATGAGATGAGAGAGATGAGCA 1333
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 387 AGCATGAGGGGCTGCCGAGACCCCTCATGCTGATGAGATGAGAGAGATGAGCA 424
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1334 TCATGCTGTAGGAGAGAGAGAGCTCTGTAAGACCTTTAAAGGTCGGTGTAG 1393
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 425 ----- 424

QY 1394 GCGTGGGGGTCAGAGACCTTCACCTCTTCCAGAGAGCTTCCCTGCGCAC 1453
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 425 ----- 424

QY 1454 CATCCCATCATGAGGATCGTGTGCTGGCTGTTGCTCTTGCAGCTGTAGTCACTGAGAC 1513
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 445 CATCCCATCATGAGGATCGTGTGCTGGCTGTTGCTCTTGCAGCTGTAGTCACTGAGAC 504
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1514 TCGGCTGGCTGCTGCTGTGAGAGAGAGCTCAGTAAGG-AAAGGGTGCAGATG 1572
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 505 TCGGCTGGCTGCTGCTGTGAGAGAGAGCTCAGTAAGG-AAAGGGTGCAGATG 564
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1573 GGGTCTAGTTTCTGTCCACTGGGGGTTTCAAGCCCAAGTAGAAGTGTGCCCTGCC 1632
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 565 GGGTCTAGTTTCTGTCCACTGGGGGTTTCAAGCCCAAGTAGAAGTGTGCCCTGCC 624
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1633 TGTGTACTGGAGACCACTCAGACTCATGAGCTGAGCTGAGCTGGGCTGTGTGCCA 1692
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 625 TGTGTACTGGAGACCACTCAGACTCATGAGCTGAGCTGAGCTGGGCTGTGTGCCA 684
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QY 1693 GCACCTTCTGTTTGTAAACACCTGTGACATGAAGAGAGATATTAATCTGTATGAT 1752
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Db 685 GCACCTTCTGTTTGTAAACACCTGTGACATGAAGAGAGATATTAATCTGTATGAT 744
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1753 TGTAGTAGTGGGAGCTGATCCAGTATCAAGGT--CAGGAGAGAGTCCCTGTGGTAA 1810
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 745 GGGAGGTGAT--GGGAGCTGATCCAGAGTCAAGTCAAGGAGGAAAGTCCCT----- 796
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1811 GACGAGCTTAGAGAGGAGCACTGTGTGAGAGACCACTCTGCTTCTTCTTCTCTGA 1870
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 797 GAGGACCTTCAGAGAGGCGGTGTGTCAGAGACCAACCTGTTCTTCATGTTCTTGA 856
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1871 T--CGCCCTGGGCTGAGAGCACATTTCTGSAACCTCTCGAGGTCACACTAGA 1928
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 857 TCCGCGCCCTGGGCTGAGAGCACATTTCTGSAACCTCTCTGAGGTCACACTAGA 916
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1929 GGTTCCTCTAGGACCTCATGGCCCTCCACCTTCTG 1966
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 917 GGTTCCTCTAGGACCTCATGGCCCTCCACCTTCTG 953
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
BQ711975      950 bp      mRNA      linear      EST 16-JUL-2002
LOCUS
DEFINITION
AGENCOURT_7975897 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214729
5', mRNA sequence.
ACCESSION
BQ711975
VERSION
BQ711975.1 GI:21850874
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 950)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/MLM at:
http://lmage.llnl.gov
Plate: LMC2382 row: 1 column: 02
High quality sequence stop: 571.
Location/Qualifiers
1..950
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/clone="IMAGE:6214729"
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/lab_host="DH10B (phage-resistant)"
/Note="Organ: spleen; Vector: pOT87; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC library."
BASE COUNT      192 a      278 c      257 g      223 t
ORIGIN

Query Match      17.9%; Score 437; DB 14; Length 950;
Best Local Similarity 80.4%; Pred. No. 3.3e-102;
Matches 589; Conservative 0; Mismatches 130; Indels 14; Gaps 6;

QY 1434 GAGCAGTCTTCCCTGCCACACATCCCATCATGATGCTGTGCTGCTGCTCTT 1493
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Db 88 GAGCAGTCTTCCCTGCCACACATCCCATCATGATGCTGTGCTGCTGCTCTT 147
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1494 GCACCTATCTACTGAGAGTGGGCTGCTGCTGTCTGTGAGAGAGAGAGCTCAGGT 1553
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Db 148 GGAAGCTGTATCTCTGAGAGTGGGCTGCTGCTGTGATGTGAGAGAGAGAGCTCAGGT 207
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QY 1554 AAGGAGGGGCTGACAAAGTGTGAGTTTCTTCTCCACTGGGGGTTTCAAGCCCA 1613
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Db 208 GGGAGAGGATGA--AGGCTGGCTCTAGATTTCTCTCACTGAGGTTCCAGACCCA 266
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SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 732)
Xiao, H., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, O., Cai, T., Zhang, X., Shen, K., Lu, G., Fu, F., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z. and Han, Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
21625106
JOURNAL MEDLINE
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhanjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
1. 732
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/clone="GKASD09"
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/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"
BASE COUNT 141 a 185 c 197 g 205 t 4 others
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Best Local Similarity 78.9%; Pred. No. 4.2e-94;
Matches 624; Conservative 0; Mismatches 92; Indels 75; Gaps 9;
QY 1579 GAGTTTCTTGTCCACGCGGGGTTTCAGGCCCGAGTAGACGTCGTCGCTGCTTA 1638
DB 1 GAGATTTCTTGTCTCTAGAGGGTTCCAGACCCAGGTAGAGTGTGCTGCTGCTTA 60
QY 1639 CTGGAGACACCATCCACTCATGTGGCCCTACCCAGCTGGCCCTGTGTCACAGCCT 1698
DB 61 CTGGAGACACCATCCACTCATGTGGCCCTACCCAGCTGGCCCTGTGTCACAGCCT 120
QY 1699 TCTCTTTTGAAGACCTGTGACATGAGAGAGATTTATACCTTGATGATTTAGT 1758
DB 121 ACTCTTTTGAAGACCTGTGACATGAGAGAGATTTATACCTTGATGATTTAGT 176
QY 1739 GATGGGACCTGATGCCAGTATACAGGT--CAGGAGAGGTCCCTGCTAAGACAGA 1816
DB 177 GAT--GGGACCTGATGCCAGTATACAGGTCAAGGAGGAGTCCCT-----GAGGAC 228
QY 1817 CCTTAGGAGGCGAGTTGGTCAGAGACCCACATCGCTTCTGTTTTCCTGAT--CGC 1874
DB 229 CTTCAGAGAGGCGGTGGTCCAGAGACCCACATCGCTTCTGATGTTTCTGATCCGCC 288
QY 1875 CCTGGGCTGACGTACACATTTCTGAAACTTCTGAGGCTCAAGACTAGAGGTTCC 1934
DB 289 CCTGGGCTGACGTACACATTTCTGAAACTTCTGAGAGCTCAAGACTAGAGGTTCC 348
QY 1935 TCTAGACCTATGAGCCCTGACCTTCTGAGCCCTGACAGACATTTTCTTCCACAG 1994
DB 349 TCTAGACCTATGAGCCCTGAGCTCTTCTGATCTCAAGACATTTTCTTCCACAG 408
QY 1995 ATTGAAGAGAGGAGACTACTCTCAAGCTGCAAGTAAGTAAGAGAGGCTGATCCCTGA 2054
DB 409 ATAGGAA----- 415
QY 2055 GATCCTTGGAGATCTGTGTTGGAG--CAATGGGAGAGTCAACCAACCCACATTTCTC 2113

DB 416 -ATCAGGAGATTTGTGTGGAGCCGTGGGGAGCTACCCACCCACATTTCTC 474
QY 2114 CTCTGGCCACA--TCTCCTGTGCTCTGACACAGAGTGTGTTTGTCTCTAGAGCAG 2172
DB 475 CTCTAGCCACANTCTCTGTGGATCTGACAGANTTGTGTTTGTCTTACCCAGCAG 534
QY 2173 TGACATGGCCAGGCGCTCAATGATGTCTCAACGCTGTAAAGTCAACCCGGGGGG 2232
DB 535 TGACAGGCCAGGCGCTCAATGATGTCTCAACGCTGTAAAGTCAACGCTGTGAGG 594
QY 2233 CTGATGTGTGGGTGTGTTGAGGGGAACAGGACATATGCTGTAGAGGTTCTTT 2292
DB 595 CTGATGTGTGGGTGTGTTGAGGGGAACAGGACATATGCTGTAGAGGTTCTTT 654
QY 2293 GACTTCATGATATGACATGATGATGGCTGTAAATGTCAACCCCTCACTGAGCTGA 2352
DB 655 GCATGATGATATGACATGATGATGGCTGTAAATGTCAACCCCTCACTGAGCAGA 711
QY 2353 TATGAATTTGT 2363
DB 712 TCCATTTTGT 722
RESULT 11
AG094772/C 655 bp DNA linear GSS 03-NOV-2001
LOCUS Pan troglodytes DNA, clone: PTB-095K06.R, genomic survey sequence.
DEFINITION AG094772
ACCESSION AG094772.1 GI:1664574
VERSION GSS.
KEYWORDS Pan troglodytes male lymphoblast DNA, clone_11b:PTB Chimpanzee Male BAC library clone:PTB-095K06.R.
SOURCE Pan troglodytes
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE 1
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Matanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
2 (bases 1 to 655)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Matanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Aseo Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: chimpanzee@riken.go.jp, URL: http://hqp.gsc.riken.go.jp/; Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the Red process and may have higher chance of clone tracking errors.
PRIMERS
Sequencing: M13Rev
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
1. 655
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/db_xref="taxon:9598"
/clone="PTB-095K06.R"
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC library"
BASE COUNT 167 a 184 c 154 g 149 t 1 others
ORIGIN
Query Match 16.3%; Score 398.8; DB 17; Length 655;
Best Local Similarity 84.4%; Pred. No. 2.3e-92;
Matches 508; Conservative 0; Mismatches 87; Indels 7; Gaps 5;

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 20:57:28 ; Search time 470 Seconds

(without alignments)
11700.808 Million cell updates/sec

Title: US-09-622-846-16

Perfect score: 2442
Sequence: 1 taccgcgagtcctccggtc.....ttgtcattccttccttgg 2442

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2442	100.0	2442	20	AA225755
2	2440.4	99.9	2442	20	AA225756
3	2420	99.1	2441	20	AA225757
4	2416.8	99.0	2441	20	AA225758
5	2395.4	98.1	148834	24	ABK83570
6	1829	74.9	4003	24	ABK84085
7	1554	63.6	3098	22	ABK18125
8	1554	63.6	3098	22	AA540421
9	1554	63.6	3098	22	AA104024

10	1554	63.6	3098	22	AAK86871	Human immune/haema
11	1551.6	63.5	4316	22	ABK83122	HLA-Cw ovarian tum
12	1551.6	63.5	4316	24	ABK97218	Gene #3716 used to
13	1423	58.3	3357	22	AA163980	Human polynucleoti
14	1420.6	58.2	3372	22	AA163979	Human polynucleoti
15	1420.6	58.2	3372	22	AA164011	Human polynucleoti
16	1415	57.9	6553	18	AA161639	HLA B27 consensus
17	1407.4	57.6	3357	22	AA163981	Human polynucleoti
18	1336.6	54.7	3874	8	AA163978	Sequence of genom
19	1333.4	54.6	1892	22	AA163975	Human polynucleoti
20	938.6	38.4	4756	22	AA163975	Human polynucleoti
21	937	38.4	4756	22	AA163974	Human polynucleoti
22	792.6	32.5	6944	24	ABK34026	Human DNA for stag
23	725.2	29.7	6944	24	ABK34027	Human DNA for stag
24	461.2	18.9	466	22	ABK42058	Human breast cell
25	461.2	18.9	466	22	ABK42059	Human breast cell
26	461.2	18.9	466	22	ABK52479	Human foetal liver
27	461.2	18.9	466	22	ABK52480	Human foetal liver
28	461.2	18.9	466	22	ABK22271	Probe #737 for gen
29	461.2	18.9	466	22	ABK22272	Probe #738 for gen
30	461.2	18.9	466	22	AAK00746	Human brain expres
31	461.2	18.9	466	22	AAK00747	Human brain expres
32	461.2	18.9	466	22	AAK26198	Human bone marrow
33	461.2	18.9	466	22	AAK26199	Human bone marrow
34	461.2	18.9	466	22	AA110829	Probe #762 for gen
35	461.2	18.9	466	22	AA110830	Probe #773 for gen
36	461.2	18.9	466	22	AA132087	Probe #774 used to
37	461.2	18.9	466	22	AA132088	Probe #774 used to
38	461.2	18.9	466	22	AA100754	Probe #745 used to
39	461.2	18.9	466	22	AA100755	Probe #746 used to
40	461.2	18.9	466	24	ABK00784	Human genome-deriv
41	461.2	18.9	466	20	AA25743	Human HLA-G gene e
42	460	18.8	460	20	AA25744	Human HLA-G gene e
43	458.4	18.8	600	20	AAK8018	Human HLA-G gene e
44	429.2	17.6	600	20	AAK8018	Histocompatibility
45	429.2	17.6	600	20	AAK38021	Histocompatibility

ALIGNMENTS

RESULT 1	AA225755	AA225755 standard; DNA; 2442 BP.
ID	AA225755	
XX	AA225755;	
AC		
XX		
DT	06-JAN-2000 (first entry)	
XX		
DE	Human HLA-G gene I-E8 and C-93 haplotype.	
XX		
KW	Human: HLA-G; pre-eclampsia; miscarriage susceptibility gene;	
KW	eclampsia; diagnosis; identification; pregnancy; miscarriage;	
KW	intrauterine growth retardation; infertility; autoimmune disease;	
KW	human leukocyte antigen-G; ss.	
XX		
OS	Synthetic.	
OS	Homo sapiens.	
XX		
PN	W09943851-A1.	
XX		
PD	02-SEP-1999.	
XX		
PF	25-FEB-1999; 99WO-IE00012.	
XX		
PR	25-FEB-1998; 98IE-0000134.	
PR	12-AUG-1996; 98IE-0000668.	
XX		
PA	(UYNA-) UNTV NAT IRELAND CORK.	
XX		
PI	O'Brien M, Bermingham J, Quane KA, Jenkins DM, McCarthy TV;	
XX	WPI; 1999-590752/50.	

XX Use of human leukocyte antigen-G (HLA-G), as a marker and in treatment
 of abnormal pregnancy or infertility and autoimmune disease
 XX
 XX Disclosure: Page 68-69; 79pp; English.

XX The present invention describes the use of a human leukocyte antigen-G
 (HLA-G) as a marker and in treatment for abnormal pregnancy or
 CC infertility and autoimmune disease. Methods from the present invention
 CC can be used for the diagnosis of susceptibility to, prevention or
 CC treatment of pre-eclampsia, eclampsia, intrauterine growth retardation,
 CC miscarriage or miscarriage-related infertility. They can also be used
 CC for treating autoimmune diseases. The present sequence represents a
 CC HLA-G gene haplotype from the present invention.

XX Sequence 2442 BP: 485 A; 659 C; 735 G; 563 T; 0 other;

Query Match 100.0%; Score 2442; DB 20; Length 2442;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACTCCGAGTCTCCGGTCTGGAGTCCACCCGAGGCGCGGACCCGCGCAGACCTTC 60
 DB 1 TACTCCGAGTCTCCGGTCTGGAGTCCACCCGAGGCGCGGACCCGCGCAGACCTTC 60
 QY 61 TACCTGGGAGAACCCCAAGGCGCTTACCAAAATCCCGGSGTGGTCCGGCGAGGG 120
 DB 61 TACCTGGGAGAACCCCAAGGCGCTTACCAAAATCCCGGSGTGGTCCGGCGAGGG 120
 QY 121 CGAGGCTCGTGGGGGGGTGACCGAGGGGGTGGGCCAGGTTTCACACCCCTCCAGTG 180
 DB 121 CGAGGCTCGTGGGGGGGTGACCGAGGGGGTGGGCCAGGTTTCACACCCCTCCAGTG 180
 QY 181 GATGATTTGGCTGCGACCTGGGGTCCGACGGACGCTCTCCGGGGGATGAACAGTATGC 240
 DB 181 GATGATTTGGCTGCGACCTGGGGTCCGACGGACGCTCTCCGGGGGATGAACAGTATGC 240
 QY 241 CTACGATGGCAAGATTACTCGCCCTGAAGAGAGACTGCGTCTCTGGACCGCAGCGGA 300
 DB 241 CTACGATGGCAAGATTACTCGCCCTGAAGAGAGACTGCGTCTCTGGACCGCAGCGGA 300
 QY 301 CACTCGGCTCAGATCTTCACAGCGCAAGTGTGAGGGCGGCAATGGTGGTGAACAAGAGAG 360
 DB 301 CACTCGGCTCAGATCTTCACAGCGCAAGTGTGAGGGCGGCAATGGTGGTGAACAAGAGAG 360
 QY 361 AGCTTACTGGAGGCGACGCTGGTGGTGGTCTCCACAGTACTGGAGAGAGGAGAGA 420
 DB 361 AGCTTACTGGAGGCGACGCTGGTGGTGGTCTCCACAGTACTGGAGAGAGGAGAGA 420
 QY 421 GATGCTGAGAGCGCGGGGTACACAGGGGCACTGGGGCGCTCCCTGATCTCTTACAGCT 480
 DB 421 GATGCTGAGAGCGCGGGGTACACAGGGGCACTGGGGCGCTCCCTGATCTCTTACAGCT 480
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 DB 481 CTCACCTGGCTTACCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 QY 541 CCTCTGGTCTGAGGAG 600
 DB 541 CCTCTGGTCTGAGGAG 600
 QY 601 TTTCTAGAGGGCCGCTCTCTCTCTGGAGCAATTAAGAGAGAGAGAGAGAGAGAGAG 660
 DB 601 TTTCTAGAGGGCCGCTCTCTCTCTGGAGCAATTAAGAGAGAGAGAGAGAGAGAGAG 660
 QY 661 GGGGAGAGCAATCCCTGAG 720
 DB 661 GGGGAGAGCAATCCCTGAG 720
 QY 721 CACCGAG 780
 DB 721 CACCGAG 780

QY 781 TGAATCAGCTCTCTGAGATCCCTTGGCTCTGCTCAGCTCAGAGAGAGAGAGAGAGAGAG 840
 DB 781 TGAATCAGCTCTCTGAGATCCCTTGGCTCTGCTCAGCTCAGAGAGAGAGAGAGAGAGAG 840
 QY 841 CCCCCGCTCAG 900
 DB 841 CCCCCGCTCAG 900
 QY 901 AGCTGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 960
 DB 901 AGCTGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 960
 QY 961 ATGTCACATCCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1020
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 DB 1021 TGAATCAGCTCTCTGAGATCCCTTGGCTCTGCTCAGCTCAGAGAGAGAGAGAGAGAGAG 1080
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 QY 1321 GAGATGAG 1380
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 DB 1441 CTTCCTGCTCAGATCCCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1500
 QY 1501 TACTCAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1560
 DB 1501 TACTCAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1560
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 QY 1681 CCGTGGTGGAG 1740
 DB 1681 CCGTGGTGGAG 1740
 QY 1741 TACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
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 QY 1801 CCGTGGTGGAG 1860
 DB 1801 CCGTGGTGGAG 1860
 QY 1861 TTTTCTGATGAG 1920

Db 1861 TTTTCCCTGATCGCCCTGGGCTCTGCACTCACAATTTTGGAATCTTGAGGGTCCAA 1920
 Qy 1921 GACAGAGAGGTTCCCTAGGACCTCATGGCCCTGTCACAGCACA 1980
 Db 1921 GACAGAGAGGTTCCCTAGGACCTCATGGCCCTGTCACAGCACA 1980
 Qy 1981 TTTTCTTCCACAGATTGAAAAGAGGAGGACTACTCTCAGGCTGCAATGATAGTAAAG 2040
 Db 1981 TTTTCTTCCACAGATTGAAAAGAGGAGGACTACTCTCAGGCTGCAATGATAGTAAAG 2040
 Qy 2041 AGGCTGATCCCTGATGATCTTGGGATTTGTTGGGAGCCATGGGGAGGCTCACCAC 2100
 Db 2041 AGGCTGATCCCTGATGATCTTGGGATTTGTTGGGAGCCATGGGGAGGCTCACCAC 2100
 Qy 2101 CCCACAATTCCTCCTCTGCGCACATCTCTGCTCTCTGACAGGTCGTTTTGTTTC 2160
 Db 2101 CCCACAATTCCTCCTCTGCGCACATCTCTGCTCTCTGACAGGTCGTTTTGTTTC 2160
 Qy 2161 TACTCTAGGACAGTACAGTCCCGCAGGGCTCTAATGTCTCTCTCAGGCTTGTAAATGTGA 2220
 Db 2161 TACTCTAGGACAGTACAGTCCCGCAGGGCTCTAATGTCTCTCTCAGGCTTGTAAATGTGA 2220
 Qy 2221 CACCCCGGGGGGCGGATGTGTTGGGTTTGTAGGGGAACAGGGGACATAGCTGTCTA 2280
 Db 2221 CACCCCGGGGGGCGGATGTGTTGGGTTTGTAGGGGAACAGGGGACATAGCTGTCTA 2280
 Qy 2281 TGAGGTTTCTTGTGACTTCAATGTATGAGATGATGGGCTGTTTAAAGTGTCCACCT 2340
 Db 2281 TGAGGTTTCTTGTGACTTCAATGTATGAGATGATGGGCTGTTTAAAGTGTCCACCT 2340
 Qy 2341 CACTGTGACTGATATGATTTGTTCATGATATTTTCTGTAGTGTAAACAGCTGCTT 2400
 Db 2341 CACTGTGACTGATATGATTTGTTCATGATATTTTCTGTAGTGTAAACAGCTGCTT 2400
 Qy 2401 GTGTGGAGTGTGAGTGAAGATTTGTTCATGCTTCCCTTTG 2442
 Db 2401 GTGTGGAGTGTGAGTGAAGATTTGTTCATGCTTCCCTTTG 2442
 RESULT 2
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 ID AA25756 standard; DNA; 2442 BP.
 XX
 AC AA25756;
 XX
 DT 06-JAN-2000 (first entry)
 XX
 DE Human HLA-G gene I-E8 and T-93 haplotype.
 XX
 KW Human: HLA-G; pre-eclampsia; miscarriage susceptibility gene;
 KW eclampsia; diagnosis; identification; pregnancy; miscarriage;
 KW intrauterine growth retardation; infertility; autoimmune disease;
 KW human leukocyte antigen-G; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN W09943851-A1.
 XX
 PD 02-SEP-1999.
 XX
 PF 25-FEB-1999; 99WO-IE00012.
 XX
 PR 25-FEB-1998; 98IE-0000134.
 PR 12-AUG-1998; 98IE-0000668.
 XX
 PA (UYNA-) UNIV NAT IRELAND CORK.
 XX
 PI O'Brien M, Beemingham J, Quane KA, Jenkins DM, McCarthy TV;
 XX WPI: 1999-590752/50.
 XX

PT Use of human leukocyte antigen-G (HLA-G), as a marker and in treatment
 PF of abnormal pregnancy or infertility and autoimmune disease -
 XX
 PS Disclosure: Page 69-70; 79pp: English.
 XX
 CC The present invention describes the use of a human leukocyte antigen-G
 CC (HLA-G) as a marker and in treatment for abnormal pregnancy or
 CC infertility and autoimmune disease. Methods from the present invention
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 CC treatment of pre-eclampsia, eclampsia, intrauterine growth retardation,
 CC miscarriage or miscarriage-related infertility. They can also be used
 CC for treating autoimmune diseases. The present sequence represents a
 CC HLA-G gene haplotype from the present invention.
 XX
 SO Sequence 2442 BP; 485 A; 658 C; 735 G; 564 T; 0 other;
 Query Match 99.9%; Score 2440.4; DB 20; Length 2442;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2441; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 TACTCCGAGTCTCCGGGTGAGATCCACCCGAGGCGCGGACCCGACACCTTC 60
 Db 1 TACTCCGAGTCTCCGGGTGAGATCCACCCGAGGCGCGGACCCGACACCTTC 60
 Qy 61 TACTGGGAGAACCCCAAGCGCTTTACCAAAATCCCGGGGTGCTCCGGCGAGG 120
 Db 61 TACTGGGAGAACCCCAAGCGCTTTACCAAAATCCCGGGGTGCTCCGGCGAGG 120
 Qy 121 CGAGGCTGGTGGGGGGGGGCTGACCGAGGGGGTGGGGCTTCTATACCTCCAGTG 180
 Db 121 CGAGGCTGGTGGGGGGGGGCTGACCGAGGGGGTGGGGCTTCTATACCTCCAGTG 180
 Qy 181 GATGATGGCTCGACCTGCGGCTCCGAGGAGCGCTCTCCGCGGATGAAAGATATGC 240
 Db 181 GATGATGGCTCGACCTGCGGCTCCGAGGAGCGCTCTCCGCGGATGAAAGATATGC 240
 Qy 241 CTACGATGGCAAGATTTACCTCGCCCTTAACAGAGAGCTGGGCTCTGAGCGGGA 300
 Db 241 CTACGATGGCAAGATTTACCTCGCCCTTAACAGAGAGCTGGGCTCTGAGCGGGA 300
 Qy 301 CACTGGGCTCGAGATCTCCAGCGCAAGTGTAGGGCGGCAATGTGGTGAACAAAGAG 360
 Db 301 CACTGGGCTCGAGATCTCCAGCGCAAGTGTAGGGCGGCAATGTGGTGAACAAAGAG 360
 Qy 361 AGCCTACCTGAGAGGACGCTGGTGAAGTGTCCACAGATACCTGGAACGGGAAGA 420
 Db 361 AGCCTACCTGAGAGGACGCTGGTGAAGTGTCCACAGATACCTGGAACGGGAAGA 420
 Qy 421 GATGCTGCAAGCGCGGGGTACCAAGGGGCGAGTGGGCGCTCCGATCTCTGTAGACT 480
 Db 421 GATGCTGCAAGCGCGGGGTACCAAGGGGCGAGTGGGCGCTCCGATCTCTGTAGACT 480
 Qy 481 CTGAGCTGTGCTAGGACCAAGAGAGGAAATGGGACCAACATGAATATGCGCCT 540
 Db 481 CTGAGCTGTGCTAGGACCAAGAGAGGAAATGGGACCAACATGAATATGCGCCT 540
 Qy 541 CCTCTGTGCTTGAAGAGAGAAATCTCTGGGTTTCCAGATCTCTGACAGAGTGA 600
 Db 541 CCTCTGTGCTTGAAGAGAGAAATCTCTGGGTTTCCAGATCTCTGACAGAGTGA 600
 Qy 601 TTTCTGAGGGCGGCTGCTGCTCTGAGCAATTAAGAGATCTCTGAGAGAGTGA 660
 Db 601 TTTCTGAGGGCGGCTGCTGCTCTGAGCAATTAAGAGATCTCTGAGAGAGTGA 660
 Qy 661 GGGGAGAGCAATCCGGAAGATGATGAGGGTCTCTTTCACCCACAGAGCTTGG 720
 Db 661 GGGGAGAGCAATCCGGAAGATGATGAGGGTCTCTTTCACCCACAGAGCTTGG 720
 Qy 721 CACGAGAGCTTTTCCCTGAGGCTTGTCTGCTCTGCTCACTCAATGTGTGGGGGTC 780
 Db 721 CACGAGAGCTTTTCCCTGAGGCTTGTCTGCTCTGCTCACTCAATGTGTGGGGGTC 780
 Qy 781 TGACTCCAGCTCTGATGCTCTGCTTGGCTTCACATCAGGTGAGAACCGAGGTCCTGCT 840

Db	1861	TTTTTCCGATACGCGCCCGGGTCTGCAGTACACATTTTTCGGAACATCTTCGAGGGTCCAA	1920		
Qy	1921	GACTAGAGAGGTTCCTCTTAGACACTCATGSCCCCTGCCACCTTTCCTG6CCTCTCACAGSACA	1980		
Db	1921	GACTAGAGAGGTTCCTCTTAGAGACCTCATG6CCCTGCACACCTTTCCTG6CCTCTCACAGSACA	1980		
Qy	1981	TTTTTCTTCCCAACATTTGAAGAAGSAGSAG6ACTCTCTCAGGCTGGCAAGTAAGTATGAAGG	2040		
Db	1981	TTTTTCTTCCCAAGATTTGAAGAAGSAGSAG6ACTCTCTCAGGCTGGCAAGTAAGTATGAAGG	2040		
Qy	2041	AGGCTGATCCCTGAGATCTTTGG6ATCTTGTTGGAGCACAATG6GAG6CTCACCCAC	2100		
Db	2041	AGGCTGATCCCTGAGATCTTTGG6ATCTTGTTGGAGCACAATG6GAG6CTCACCCAC	2100		
Qy	2101	CCCAACATTCCTCTCTG6GCAATCTCCCTG6GCTCTGACACAGT6CTGTTTTTGTTC	2160		
Db	2101	CCCAACATTCCTCTCTG6GCAATCTCCCTG6GCTCTGACACAGT6CTGTTTTTGTTC	2160		
Qy	2161	TACTCTAGGCAAGTACAGTCCCAAGG6CTCTAATGTCTCTCACAGGCTTGTAATGGA	2220		
Db	2161	TACTCTAGGCAAGTACAGTCCCAAGG6CTCTAATGTCTCTCACAGGCTTGTAATGGA	2220		
Qy	2221	CACCCCG6G6G6CCTGATGTGTGTG6GTTGTTAG6GGAACAAG6GACATAGCTGTGTA	2280		
Db	2221	CACCCCG6G6G6CCTGATGTGTGTG6GTTGTTAG6GGAACAAG6GACATAGCTGTGTA	2280		
Qy	2281	TGAGGTTTCTTTGACTTCATGATGTAATTAGACATGTGATG6GCTGTTTAAAGTGCACCCCT	2340		
Db	2281	TGAGGTTTCTTTGACTTCATGATGTAATTAGACATGTGATG6GCTGTTTAAAGTGCACCCCT	2340		
Qy	2341	CACGTGTGACGTATATGTAATTTTTCATGAATATTTTCTGTAGTGTGAACACGTG6CCT	2400		
Db	2341	CACGTGTGACGTATATGTAATTTTTCATGAATATTTTCTGTAGTGTGAACACGTG6CCT	2400		
Qy	2401	GTTGGGACCTGAGTGGCAAGATTTGTTCAAGCTTCCTTTG	2442		
Db	2401	GTTGGGACCTGAGTGGCAAGATTTGTTCAAGCTTCCTTTG	2442		
RESULT 3					
ID	AAZ25757	AAZ25757 standard; DNA; 2441 BP.			
AC	AAZ25757;				
DX	06-JAN-2000	(first entry)			
DE	Human HLA-G gene D-E8 and C-93 haplotype.				
XX	Human: HLA-G; pre-eclampsia; miscarriage susceptibility gene;				
KM	eclampsia; diagnosis; identification; pregnancy; miscarriage;				
KW	intrauterine growth retardation; infertility; autoimmune disease;				
KW	human leukocyte antigen-G; ss.				
OS	Synthetic.				
OS	Homo sapiens.				
XX	WO9943851-A1.				
XX	02-SEP-1999.				
XX	25-FEB-1999; 99WO-IR00012.				
XX	25-FEB-1998; 98IE-0000134.				
PR	12-AUG-1998; 98IE-0000668.				
XX	(UYNA-) UNIV NAT IRELAND CORK.				
XX	O'Brien M, Bermingham J, Quane KA, Jenkins DM, McCarthy TV;				
DR	WPI; 1999-590752/50.				
XX	Use of human leukocyte antigen-G(HLA-G), as a marker and in treatment				

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XX Disclosure; Page 70-71: 79pp: English.

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CC (HLA-G) as a marker and in treatment for abnormal pregnancy or
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CC treatment of pre-eclampsia, eclampsia, intrauterine growth retardation,
CC miscarriage or miscarriage-related infertility. They can also be used
CC for treating autoimmune diseases. The present sequence represents a
CC HLA-G gene haplotype from the present invention.

XX Sequence 2441 BP: 488 A; 659 C; 735 G; 559 T; 0 other:

Query Match 99.1%; Score 2420; DB 20; Length 2441;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACTCCGAGTCTCCGGGCTGGGATCCACCCGAGGCGCGGACCCCGCAGACCCCTC 60
DB 1 TACTCCGAGTCTCCGGGCTGGGATCCACCCGAGGCGCGGACCCCGCAGACCCCTC 60
QY 61 TACCTGGAGAGAACCCCAAGGCGCTTACCAAAATCCCGGGGTGGGTCCGGGCGAGG 120
DB 61 TACCTGGAGAGAACCCCAAGGCGCTTACCAAAATCCCGGGGTGGGTCCGGGCGAGG 120
QY 121 CGAGGCTGGTGGGCGGGGCTGACCGAGGCGGTGGGCGCAGGTTCTACACCCCTCAGTG 180
DB 121 CGAGGCTGGTGGGCGGGGCTGACCGAGGCGGTGGGCGCAGGTTCTACACCCCTCAGTG 180
QY 181 GATGATGGCTGCGACCTGGGGGTCCGACGAGACCTCTCTCCGGGGTATGAACAGTATGC 240
DB 181 GATGATGGCTGCGACCTGGGGGTCCGACGAGACCTCTCTCCGGGGTATGAACAGTATGC 240
QY 241 CTACAGATGGCAAGATTACTCGCCCTGAACGAGACCTCGCTCTGAGACCGCAGCGA 300
DB 241 CTACAGATGGCAAGATTACTCGCCCTGAACGAGACCTCGCTCTGAGACCGCAGCGA 300
QY 301 CACTCGGCTGAGATCTCCAAAGCCCAAGCTGAGCGGCGCAATGTGGTGAACAAAGAG 360
DB 301 CACTCGGCTGAGATCTCCAAAGCCCAAGCTGAGCGGCGCAATGTGGTGAACAAAGAG 360
QY 361 ACCCTACTGAGGCGACGTCGTGAGTGGCTCCACAGATACCTTGGAGAGCGGAGGA 420
DB 361 ACCCTACTGAGGCGACGTCGTGAGTGGCTCCACAGATACCTTGGAGAGCGGAGGA 420
QY 421 GATGCTGAGGCGCGGGGTACAGGGGCGAGTGGGGCGCTCGTGAATCTCTGTAGACT 480
DB 421 GATGCTGAGGCGCGGGGTACAGGGGCGAGTGGGGCGCTCGTGAATCTCTGTAGACT 480
QY 481 CTCACGCTGGCTAGCACAGAGAGAGAAAATGGGACCAACTAGATATCGCCCT 540
DB 481 CTCACGCTGGCTAGCACAGAGAGAGAAAATGGGACCAACTAGATATCGCCCT 540
QY 541 CCCTCTGGCTGAGGGGAGAGAAATCCCTGGGTTCCAGATCTGATCCAGAGAGTA 600
DB 541 CCCTCTGGCTGAGGGGAGAGAAATCCCTGGGTTCCAGATCTGATCCAGAGAGTA 600
QY 601 TTCTGAGGCGCGCTCTCTCTGAGCAATTAAAGGATGAAGTCTGTAGGAGATGA 660
DB 601 TTCTGAGGCGCGCTCTCTCTGAGCAATTAAAGGATGAAGTCTGTAGGAGATGA 660
QY 661 GGGGAGAGCAATCCCTGAGAGAGATGATGAGGCTTCCCTTGAAGCCGACAGAGCTTGG 720
DB 661 GGGGAGAGCAATCCCTGAGAGAGATGATGAGGCTTCCCTTGAAGCCGACAGAGCTTGG 720
QY 721 CACCAAGAGATTTTCCCTCAGGCTTGTCTCTGCTCAGACTCAATGTGTGTGGGGTTC 780
DB 721 CACCAAGAGATTTTCCCTCAGGCTTGTCTCTGCTCAGACTCAATGTGTGTGGGGTTC 780
QY 781 TGAGCTCAGCTCTCTGAGTCCCTTGGCTCAGTCAAGGTCAGAGCGGAGGCTCTGCT 840
DB 781 TGAGCTCAGCTCTCTGAGTCCCTTGGCTCAGTCAAGGTCAGAGCGGAGGCTCTGCT 840

DB 781 TGAGCTCAGCTCTCTGAGTCCCTTGGCTCAGTCAAGGTCAGAGCGGAGGCTCTGCT 840
QY 841 CCCCGGCTGAGAGACTAGACTTTTCCAGAGATAGAGATTATCCAGAGTCCCGGTGTC 900
DB 841 CCCCGGCTGAGAGACTAGACTTTTCCAGAGATAGAGATTATCCAGAGTCCCGGTGTC 900
QY 901 AGAGCTGTGTGGGTTCTGTGCTCCCTTCCCGCCAGGATTCAGGTTCTTCTTCTAG 960
DB 901 AGAGCTGTGTGGGTTCTGTGCTCCCTTCCCGCCAGGATTCAGGTTCTTCTTCTAG 960
QY 961 ATGGTCAATCAGTGTCTGTGAGTGTCCATGAGATGCAAGATGCTGATTTTC 1020
DB 961 ATGGTCAATCAGTGTCTGTGAGTGTCCATGAGATGCAAGATGCTGATTTTC 1020
QY 1021 TGAGCTCTCTTCCAGAGCCCGCCCAAGACACAGTGAACACCACTGCTTGAATAT 1080
DB 1021 TGAGCTCTCTTCCAGAGCCCGCCCAAGACACAGTGAACACCACTGCTTGAATAT 1080
QY 1081 GAGGCGACCTGAGTGTGGGCTGGGCTGCTTACCTTGGGATCATAGACTGAG 1140
DB 1081 GAGGCGACCTGAGTGTGGGCTGGGCTGCTTACCTTGGGATCATAGACTGAG 1140
QY 1141 CAGCGGATGGGAGAGACAGACCCAGAGAGTGGAGCTGGAGACAGAGCTGAGG 1200
DB 1141 CAGCGGATGGGAGAGACAGACCCAGAGAGTGGAGCTGGAGACAGAGCTGAGG 1200
QY 1201 GATGGAACCTTCCAGAAAGTGGGACGCTGTGGTGTCTTGGAGAGAGAGATAC 1260
DB 1201 GATGGAACCTTCCAGAAAGTGGGACGCTGTGGTGTCTTGGAGAGAGAGATAC 1260
QY 1261 AGTGCATGTGACATGAGAGGCGTGCAGAGGCGCCGATGCTGAGATGAGTAAAGAG 1320
DB 1261 AGTGCATGTGACATGAGAGGCGTGCAGAGGCGCCGATGCTGAGATGAGTAAAGAG 1320
QY 1321 GAGATGAGAGCATATGTCTGTAGGAAAGAGAGACCTCTCTGAGACCTTAAACAG 1380
DB 1321 GAGATGAGAGCATATGTCTGTAGGAAAGAGAGACCTCTCTGAGACCTTAAACAG 1380
QY 1381 GGTGGTGGGAGGCGTGGGAGTGCAGAGACCTCAGTCACTCTCTTCCAGAGAGT 1440
DB 1381 GGTGGTGGGAGGCGTGGGAGTGCAGAGACCTCAGTCACTCTCTTCCAGAGAGT 1440
QY 1441 CTTCCTGCCCACATCCCATCATAGGATATGCTGTGCTGGCTGTGCTTGCAGCTG 1500
DB 1441 CTTCCTGCCCACATCCCATCATAGGATATGCTGTGCTGGCTGTGCTTGCAGCTG 1500
QY 1501 TAGTCACTGAGCTGCGGCTGCTGCTGTGTGAGAAAGAAAGAGCTCAGTAAGAG 1560
DB 1501 TAGTCACTGAGCTGCGGCTGCTGCTGTGTGAGAAAGAAAGAGCTCAGTAAGAG 1560
QY 1561 GGGTGAACAAGTGGGCTGTAGATTTCTGTGCTCCACATGAGGCTTCAAGCCAGTAAG 1620
DB 1561 GGGTGAACAAGTGGGCTGTAGATTTCTGTGCTCCACATGAGGCTTCAAGCCAGTAAG 1620
QY 1621 GTGTGCTGCTGAGTGTACTGAGAGACCATCACTATGAGGCTTACCCAGCTGGG 1680
DB 1621 GTGTGCTGCTGAGTGTACTGAGAGACCATCACTATGAGGCTTACCCAGCTGGG 1680
QY 1681 CCCTGTGTGCGACACCTTCTCTTTTGTAAAGACCTGTGACATTAAGAGACATTTAT 1740
DB 1681 CCCTGTGTGCGACACCTTCTCTTTTGTAAAGACCTGTGACATTAAGAGACATTTAT 1740
QY 1741 TACCTGATGATGTGTATGATGAGGAGCTGATCCAGTAATCAAGTCAAGAGAGTTC 1800
DB 1741 TACCTGATGATGTGTATGATGAGGAGCTGATCCAGTAATCAAGTCAAGAGAGTTC 1800
QY 1801 CTTGGCTAAGAGACACTTATAGAGAGAGTGTGTGAGAGACCACTTCTTCTTCTG 1860
DB 1801 CTTGGCTAAGAGACACTTATAGAGAGAGTGTGTGAGAGACCACTTCTTCTTCTG 1860
QY 1861 TTTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
DB 1861 TTTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920

Qy	841	CCCCCGCCAGAGACTAGACTTTCACAGAGATTAGAGATTATCCAGAGTGCCTGCTCC	900
Db	841	CCCCCGCTCAGAGACTAGAACTTTCAGAGAAATAGAGATTATCCAGAGTGCCTGCTCC	900
Qy	901	AGAGCTGCTGTGGGTTTCTAGCTCCCTTCCCAAGCCAGGATATCTGGTCAATCTTAGG	960
Db	901	AGAGCTGCTGTGGGTTTCTAGCTCCCTTCCCAAGCCAGGATATCTGGTCAATCTTAGG	960
Qy	961	ATGCTCACAATCCAGSTGCTGCTGAGATGTCCTATAGAGATGCAAGTGGTGAATTTTC	1020
Db	961	ATGCTCACAATCCAGSTGCTGCTGAGATGTCCTATAGAGATGCAAGTGGTGAATTTTC	1020
Qy	1021	TGACTCTTTCCTTTAGAGACCCCCCAAGACACAGTGACCCACACCCTGTCTTGACAT	1080
Db	1021	TGACTCTTTCCTTTAGAGACCCCCCAAGACACAGTGACCCACACCCTGTCTTGACAT	1080
Qy	1081	GAGGCCACCTGAGTGTCTGAGCCCTGTGGCTTCTACCTGCGGAGATCATAGACCTGG	1140
Db	1081	GAGGCCACCTGAGTGTCTGAGCCCTGTGGCTTCTACCTGCGGAGATCATAGACCTGG	1140
Qy	1141	CACCGGATGGGAGAGACACAGACCAGAGACGTGGAGCTGTGGAGACACAGCCCTGAGG	1200
Db	1141	CACCGGATGGGAGAGACACAGACCACAGACGTGGAGCTGTGGAGACCAAGCCCTGAGG	1200
Qy	1201	GATGGAACCTTCCAGAAAGTGGGAGCTGTGGTGTGCTTGTGGAGAGAGACAGATAC	1260
Db	1201	GATGGAACCTTCCAGAAAGTGGGAGCTGTGGTGTGCTTGTGGAGAGAGACAGATAC	1260
Qy	1261	ACGTGCAATGTGACATGAGGGGCTCCGAGCCCTCATAGTCAGATGAGATGAATAGAG	1320
Db	1261	ACGTGCAATGTGACATGAGGGGCTCCGAGAGCCCTCATAGTCAGATGAGATGAATAGAG	1320
Qy	1321	GGAGATGGAGCATATGTCTGTAGGAGAAACAGAGACCTCTCTGAAGACCTTTAAAG	1380
Db	1321	GGAGATGGAGCATATGTCTGTAGGAGAAACAGAGACCTCTCTGAAGACCTTTAAAG	1380
Qy	1381	GGTGGGTGTAGGGCTGGGGGCTCAGAGACCCATCACTCACTCCCTTCCAGACACT	1440
Db	1381	GGTGGGTGTAGGGCTGGGGGCTCAGAGACCCATCACTCACTCCCTTCCAGACACT	1440
Qy	1441	CTTCCCTGCCACCACTCCCATCATGGGATGTGCTGTGGCCTGGTTGCTCTTGACGCTG	1500
Db	1441	CTTCCCTGCCACCACTCCCATCATGGGATGTGCTGTGGCCTGGTTGCTCTTGACGCTG	1500
Qy	1501	TATCTCATCTGAGACTCGGCTGCTGTCTGTGGAGAAAGAAAGACTCAGATGAAGAG	1560
Db	1501	TATCTCATCTGAGACTCGGCTGCTGTCTGTGGAGAAAGAAAGACTCAGATGAAGAG	1560
Qy	1561	GGGTGACAGTGGGCTGAGATTTTCTGTCCACTGGGGGCTTTCAAGCCCCAGGTAGA	1620
Db	1561	GGGTGACAGTGGGCTGAGATTTTCTGTCCACTGGGGGCTTTCAAGCCCCAGGTAGA	1620
Qy	1621	GTTGCTCCCTGCTGTTACTGTGGAGACACATCCATCATGGGCTTACCACAGCTGGG	1680
Db	1621	GTTGCTCCCTGCTGTTACTGTGGAGACACATCCATCATGGGCTTACCACAGCTGGG	1680
Qy	1681	CCCTGTGTCCAGACCTTCTCTTTGTAAAGCACTGTGACCAATGAAGACAGATTAT	1740
Db	1681	CCCTGTGTCCAGACCTTCTCTTTGTAAAGCACTGTGACCAATGAAGACAGATTAT	1740
Qy	1741	TACCTTGAATTTGATAGTATGGGAGCTGTATCCAGTAATACAGGTCAAGAGAAAGTTC	1800
Db	1741	TACCTTGAATTTGATAGTATGGGAGCTGTATCCAGTAATACAGGTCAAGAGAAAGTTC	1800
Qy	1801	CTGTGCTAAGGACACACTTGTAGAGGGCAATGTATCCAGTAATACAGGTCAAGAGAAAGTTC	1860
Db	1801	CTGTGCTAAGGACACACTTGTAGAGGGCAATGTATCCAGTAATACAGGTCAAGAGAAAGTTC	1860
Qy	1861	TTTTTCTCATATGCCCTGGGCTGTGACATCAACATTTCTGGAAACTTCTCGAGGGTCCAA	1920
Db	1861	TTTTTCTCATATGCCCTGGGCTGTGACATCAACATTTCTGGAAACTTCTCGAGGGTCCAA	1920

Oy	1921	GCTAGAGAGTTCCTCTTGAGACATCAGCCGCGACCTTTCGGCTCTCAGACACA	1980
Oy	1921	GCTAGAGAGTTCCTCTTGAGACATCAGCCGCGACCTTTCGGCTCTCAGACACA	1980
Db	1921	GACTAGAGAGTTCCTCTTGAGACATCAGCCGCGACCTTTCGGCTCTCAGACACA	1980
Oy	1981	TTTTTCTTCCACAGATTGAAAAGGAGGAGCTACTCTCAGCTGCAAGTAATGAAAG	2040
Db	1981	TTTTTCTTCCACAGATTGAAAAGGAGGAGCTACTCTCAGCTGCAAGTAATGAAAG	2040
Oy	2041	AGGCTATCCCTGAGATCTCTGGGATCTTGTGTGGAGCCATGGGGGAGCTCACCCAC	2100
Db	2041	AGGCTATCCCTGAGATCTCTGGGATCTTGTGTGGAGCCATGGGGGAGCTCACCCAC	2100
Oy	2101	CCGACAATTCTCTCTTGCCACATCTCCTGTGTGTGTGTGTGTGTGTGTGTGTGT	2160
Db	2101	CCGACAATTCTCTCTTGCCACATCTCCTGTGTGTGTGTGTGTGTGTGTGTGTGT	2160
Oy	2161	TACTCTAGGAGAGTGAACAGTGGCCGAGGCTCTTAATGTGTCTCAGCGCTTGTAAATGA	2220
Db	2161	TACTCTAGGAGAGTGAACAGTGGCCGAGGCTCTTAATGTGTCTCAGCGCTTGTAAATGA	2220
Oy	2221	CACCCGAGGAGGAGCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2280
Db	2221	CACCCGAGGAGGAGCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2280
Oy	2281	TGAGGTTCTCTTGACCTCAATGATTTAGATGTGATGTGGCGTTTAAAGTCCACCCCT	2340
Db	2281	TGAGGTTCTCTTGACCTCAATGATTTAGATGTGATGTGGCGTTTAAAGTCCACCCCT	2340
Oy	2341	CACGTGACTGATATGAAATTTGTTTCATGAAATATTTTCTGTAGTGTGAACAGCTGCCCT	2400
Db	2341	CACGTGACTGATATGAAATTTGTTTCATGAAATATTTTCTGTAGTGTGAACAGCTGCCCT	2400
Oy	2401	GTTGTGGAGCTGAGTGGCAAG 2420	
Db	2401	GTTGTGGAGCTGAGTGGCAAG 2420	
RESULT 5			
ABK83570/C			
ID	ABK83570	standard; cDNA: 148834 BP.	
XX	XX		
AC	ABK83570:		
XX	XX		
DT	14-AUG-2002	(first entry)	
XX	XX		
DE	Human cDNA differentially expressed in granulocytic cells #141.		
XX	XX		
KW	Human; ss: granulocytic cell; DNA chip: bacterial infection;		
KW	fungal infection; parasitic infection; protozoal infection;		
KW	viral infection; sterile inflammatory disease; psoriasis;		
KW	rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;		
KW	cardiac reperfusion injury; renal reperfusion injury; AIDS;		
KW	adult respiratory distress syndrome; inflammatory bowel disease;		
KW	Crohn's disease; ulcerative colitis; periodontal disease;		
KW	granulocyte activation; chronic inflammation; allergy.		
XX	OS	Homo sapiens.	
XX	XX		
PN	W0200228999-A2.		
PD	11-APR-2002.		
XX	XX		
PF	03-OCT-2001; 2001WO-US30821.		
XX	XX		
PR	03-OCT-2000; 2000US-237189P.		
XX	XX		
PA	(GENE-) GENE LOGIC INC.		
XX	XX		
PI	Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;		
DR	WPI; 2002-435328/46.		
PT	Detecting granulocyte activation by detecting differential expression		

PT of genes associated with granulocyte activation, which serves as
 PT diagnostic markers that is useful for monitoring disease states and
 PT drug toxicity

PS Claim 1; SEQ ID No 141; 114pp; English.

XX The invention relates to detecting (M1) granulocyte (GC) activation
 CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
 CC DNA chip analysis as given in the specification, and comparing
 CC the expression level to an expression level in an unactivated
 CC GC, where differential expression of Gs is indicative of GCA.
 CC Also included are modulating (M2) Gs by contacting GC with an agent
 CC that alters the expression of at least one gene in Gs; (2) screening (M3)
 CC for an agent capable of modulating GCA or an inflammation (especially
 CC chronic) in a tissue, an allergic response in a subject, exposure of a
 CC subject to a pathogen or sterile inflammatory disease using the
 CC gene expression profile; (3) detecting (M4) an inflammation (especially
 CC chronic) in a tissue, an allergic response in a subject, exposure of a
 CC subject to a pathogen or sterile inflammatory disease, by detecting the
 CC level of expression in a sample of the tissue of gene(s) from Gs, where
 CC the level of expression of the gene is indicative of inflammation;
 CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
 CC an allergic response in a subject, exposure of a subject to a pathogen
 CC or sterile inflammatory disease, by contacting a tissue having
 CC inflammation with an agent that modulates the expression of gene(s)
 CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
 CC modulating Gs; M3 is useful for screening an agent capable of modulating
 CC GCA preferably in an inflammation in a tissue; M4 is useful for
 CC detecting an inflammation (especially chronic) in a tissue, an allergic
 CC response in a subject, exposure of a subject to a pathogen or sterile
 CC inflammation (especially chronic) or in a tissue, an allergic
 CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
 CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
 CC reperfusion injury, ARDS, adult respiratory distress syndrome,
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
 CC periodontal disease; also bacterial infection, viral infection,
 CC parasitic infection, protozoal infection, fungal infection and M5 is
 CC useful for treating one of the above conditions. The present
 CC sequence represents a gene differentially expressed in granulocytes.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pcl_sequences.

XX Sequence 148834 BP: 38942 A: 33672 C: 34501 G: 41719 T: 0 other:

Query Match 98.1%; Score 2395.4; DB 24; Length 148834;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2419; Conservative 0; Mismatches 1; Indels 3; Gaps 2;

QY 1 TACTCCGAGTCTCCGGGTCTGGATCCACCCGAGGCGCGGAGCCGCCAGACCTC 60
 Db 12138 TACTCCGAGTCTCCGGGTCTGGATCCACCCGAGGCGCGGAGCCGCCAGACCTC 12079
 QY 61 TACTCCGAGTCTCCGGGTCTGGATCCACCCGAGGCGCGGAGCCGCCAGACCTC 120
 Db 12078 TACTCCGAGTCTCCGGGTCTGGATCCACCCGAGGCGCGGAGCCGCCAGACCTC 12019
 QY 121 CGAGGCTCGGTGGGCGGCTGACGACGAGGCGGAGGCTTTCACACCTCCCAATG 180
 Db 12018 CGAGGCTCGGTGGGCGGCTGACGACGAGGCGGAGGCTTTCACACCTCCCAATG 11599
 QY 181 GATGATTTGGTCTGACCTGGGCTGACGAGGAGCTCTCTCCGCGGATTAAGACATATGC 240
 Db 11958 GATGATTTGGTCTGACCTGGGCTGACGAGGAGCTCTCTCCGCGGATTAAGACATATGC 11899
 QY 241 CTACGATGGGAGGATTTACTCGCTTGAAGGAGGAGCTGCTCTGAGACCGGAGGGA 300
 Db 11898 CTACGATGGGAGGATTTACTCGCTTGAAGGAGGAGCTGCTCTGAGACCGGAGGGA 11839
 QY 301 CACTGCGGCTCAAGTCTCAAGGCGAAGTGTGAGCGCGCAATGTGTCTGAAACAAGAG 360
 Db 11838 CACTGCGGCTCAAGTCTCAAGGCGAAGTGTGAGCGCGCAATGTGTCTGAAACAAGAG 11779

QY 361 AGCTTACCTGGAGGCGACGTGCGTGGAGTGGCTCCACAGATACCTGGAGAGGGAAGCA 420
 Db 11778 AGCTTACCTGGAGGCGACGTGCGTGGAGTGGCTCCACAGATACCTGGAGAGGGAAGCA 11719
 QY 421 GATGCTGACGCGCGGGGTACAGGGGAGTGGGGCGCTCCCTGATCTCTGTAGACCT 480
 Db 11718 GATGCTGACGCGCGGGGTACAGGGGAGTGGGGCGCTCCCTGATCTCTGTAGACCT 11659
 QY 481 CTCAGCTGCGCTTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
 Db 11658 CTCAGCTGCGCTTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 11599
 QY 541 CCTCTGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
 Db 11598 CCTCTGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 11539
 QY 601 TTCTGAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 Db 11538 TTCTGAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 11479
 QY 661 GGGGAGACATCTCTGGAAGACTGATCAGGGGTTCCTTTGACCCCAAGACGCTTGG 720
 Db 11478 GGGGAGACATCTCTGGAAGACTGATCAGGGGTTCCTTTGACCCCAAGACGCTTGG 11419
 QY 721 CACGAGACTTTTCCCTCAGGCGCTTGTCTGTGCTCAGCAGTATGTGTGGGGATC 780
 Db 11418 CACGAGACTTTTCCCTCAGGCGCTTGTCTGTGCTCAGCAGTATGTGTGGGGATC 11359
 QY 781 TGACTCAGCTCTCTGAGTCCCTTGGCTCCACTCAGGTGAGACCGGAGGCTCCCTGCT 840
 Db 11358 TGACTCAGCTCTCTGAGTCCCTTGGCTCCACTCAGGTGAGACCGGAGGCTCCCTGCT 11299
 QY 841 CCCCCCTCAGAGACTAGAACTTTTCAAGAGAAATAGAGATATCCAGGCGCGCTGTC 900
 Db 11298 CCCCCCTCAGAGACTAGAACTTTTCAAGAGAAATAGAGATATCCAGGCGCGCTGTC 11239
 QY 901 AGCTGTGCTCTGGGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 Db 11238 AGCTGTGCTCTGGGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 11179
 QY 961 ATGCTCAGTCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
 Db 11178 ATGCTCAGTCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 11119
 QY 1021 TGACTCTTCTTTCAGACCCCTCCCAAGACACAGTGAACCCACCTGCTTGTGACTAT 1080
 Db 11118 TGACTCTTCTTTCAGACCCCTCCCAAGACACAGTGAACCCACCTGCTTGTGACTAT 11059
 QY 1081 GAGGCGACCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
 Db 11058 GAGGCGACCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 10999
 QY 1141 CAGCGGATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
 Db 10998 CAGCGGATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 10939
 QY 1201 GATGAGACCTTCCAGAAAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260
 Db 10938 GATGAGACCTTCCAGAAAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 10879
 QY 1261 ACCTGCGATGTCAGCAGTGAAGGAGGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
 Db 10878 ACCTGCGATGTCAGCAGTGAAGGAGGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 10819
 QY 1321 GAGGATGGAGGAGGATGCTGTTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1380
 Db 10818 GAGGATGGAGGAGGATGCTGTTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 10759
 QY 1381 GGTGCTGTGAGGCTGGGGGTGAGAGACCTCCTACCTTCTCTTCCAGAGAGCT 1440
 Db 10758 GGTGCTGTGAGGCTGGGGGTGAGAGACCTCCTACCTTCTCTTCCAGAGAGCT 10699
 QY 1441 CTTCCTTCCGACATCCCATCATGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500

XX Sequence 4003 BP: 797 A; 1116 C; 1204 G; 886 T; 0 other;

Query Match 74.9%; Score 1829; DB 24; Length 4003;
Best Local Similarity 88.3%; Pred. No. 0;
Matches 2181; Conservative 0; Mismatches 245; Indels 45; Gaps 16;

3 CTCCGAGTCTCCGGATCTGGATTCACACCCGAGGCGCGGACCCGACAGCCTCTA 62
Db 1061 CCCCTGATCTCCGGTCTCAGATTCAGACCCGAGGCTGGCGGACCTGCAAGATCTCTCA 1120
Qy 63 CCTGGGAACACCCCAAGGCGCTTTA-----CCAAATCCCG 100
Db 1121 CCCGGAGAGCCCAAGGCGCTTTACCTGTTTCATCTTCAGTTGAGGCCAAATATCTCG 1180
Qy 101 CGGATGGTCCGGGCGAGGCGGCTGGTGGCGGGCTGACGAGGAGGTTGGGCGCA 160
Db 1181 CAGTTGCTAGGGGCGGGCCAGGGGCTGGGGGCTGACCGGGGAACTGGGCGCA 1240
Qy 161 GATTCTCACACCTTCAGTGTATTTGCTGGACCTGGGGTCCGACGAGCCTCTCTC 220
Db 1241 GGTATTCACATCTTCACAGGATTTTGGCTGCGACCTGGGGCCGACAGGCGCTCTCTC 1300
Qy 221 CGCGGATGAACAGATGCTTACGATGCAAGGATTAACCTGCGCTGAAAGAGGACCTG 280
Db 1301 CGCGGATGAAGAGATGCTTACGATGCAAGGATTAACCTGCGCTGAAAGAGGACCTG 1360
Qy 281 CGCTCTCGACCGGAGGAGACCTGGGCTCAGATCTCCAGGCGCAAGTGTAGGGCGCC 340
Db 1361 CGCTCTCGACCGGAGGAGACCTGGGCTCAGATCTCCAGGCGCAAGTGTAGGGCGCC 1420
Qy 341 AATGAGCTGAACAAGAGAGACCTTACCTGAGGAGGACGCTGCTGAGAGTGTGACACAA 400
Db 1421 AATGAGCTGAACAAGAGAGACCTTACCTGAGGAGGACGCTGAGAGTGTGCTCCGACA 1480
Qy 401 TACCTGAGAGAGAGAGAGATGCTGACAGCGCGGGTACAGGAGGCAATGGGGCGCT 460
Db 1481 CACCTGAGAGAGAGAGAGATGCTGACAGCGCGGGTACAGGAGGCAATGGGGCGCT 1540
Qy 461 CCCTGATCTCTGAGACCTCTCAGCCTGGCTGACCAAGAGAGAGAGAAATGGGAC 520
Db 1541 GCTGATCTCTGAGATCTCCGGGCTGGGCTGCGACAAAGAGAGAGAAATGGGAAA 1600
Qy 521 CACACTGAGAGATGCGCTCTGCTGCTGCTGAGGAGAGAGATCTCTGCTGCTTCCA 580
Db 1601 CACCTGAGAGATGCGCTCTGCTGCTGCTGAGGAGAGAGATCTCTGCTGCTTCCA 1660
Qy 581 GATCTGTACAGAGAGATGCTGTAGAGGCGCGCTGCTCT--CTGGACAATTAAGG 638
Db 1661 GATCTGTATCAGAGATGCTGTAGAGGCGCGCTGCTCTCTCTGAGGACAATTAAGG 1720
Qy 639 ATGAGATCTGTAGAGAGATGAGGAGAGACATCTCTGAGAGAGATGAGAGGTTCC 698
Db 1721 ATGAGATCTGTAGAGAGATGAGGAGAGACATCTCTGAGAGAGATGAGAGGTTCC 1780
Qy 699 TTGAGCCCAAGACGCTT--GACACAGACATTTCCCTCAGGCGCTTGTCTGCT 757
Db 1781 TTTCACCCCAAGACGCTTGTGGGACACGACATTTCTCCGCGGCTTGTCTGCT 1840
Qy 758 CACACTGAGATGTTGGGGTGTGACCTCAGCTCCTCTGAGTCCCTGGGCTGCACTCA 817
Db 1841 CACACTCAA--TGTGTGAGATGTGACTCCAGCTCCTCTGAGTCCCTGGGCTGCACTCA 1898
Qy 818 GGTCAAGAACCGGAGTCTCTCCCGCTCAGAGACTAAGAACTTCCAGAGAAATAGA 877
Db 1899 GATTATCCAGAGTCCGCTGTCAGAGGCTGTGGTCTGTGCTCTGCTCTCCAGAG 937
Qy 878 GATTATCCAGAGTCCGCTGTCAGAGGCTGTGGTCTGTGCTCTGCTCTCCAGAG 937
Db 1959 GATTATCCAGAGTCCGCTGTCAGAGGCTGTGGTCTGTGCTCTGCTCTCCAGAG 2018
Qy 938 CAGTATCTGTCTATTTAGATGTGATCATTCAGAGTCTCTGAGAGTGTCCATGAG 997
1111 11 1111111111 1111111111

Db 2019 CAGGTGCTATTTCA---TCAGGATGTGCAT--GGGCGTCTGGGGTGTCCATGAG 2073
Qy 998 AGATGCAAAATGCTGTAATTTTCTGACTCTCTCTTTCAGA--CCCCCAACACACAGT 1056
Db 2074 GAATGCAAAATGCTGTAATTTTCTGACTCTCTCTTTCACACCCCCCAACACACAGT 2133
Qy 1057 ACCCAGCACCTGTCTTTGACTATGAGGCGCACCTGAGTGGTGGGCTGGGCTTCTAC 1116
Db 2134 ACCCAGCCCCCTCTGACAT--GAGGCATTAAGAGGCTCTGTGGTCTGGGCTTCTAC 2190
Qy 1117 CTTGCGAGATTCATCTGACTGTGCGAGCGGATGGGAGAGACCAACCCAGAGCTGGAG 1176
Db 2191 CTTGCGAGATTCATCTGACTGTGCGAGCGGATGGGAGAGACCAACCCAGAGCTGGAG 2250
Qy 1177 CTTGCGAGACCGGCTGAGGAGTGAACCTTCCAGAAATGGGCGAGCTGTGTGTG 1236
Db 2251 CTTGCGAGACCGGCTGAGGAGTGAACCTTCCAGAAATGGGCGAGCTGTGTGTG 2310
Qy 1237 CTTCTGAGAGAGACAGAGATACAGTCCATGTTCAGACATGAGAGGCTCCCGAGCC 1296
Db 2311 CTTCTGAGAGAGAGAGAGATACAGTCCATGTTCAGACATGAGAGGCTCCCGAGCC 2370
Qy 1297 CTTATGCTGAGATGAGTAAAGAGAGATGAGG--ATCATGTCTGTTAAGAGAAAGAG 1355
Db 2371 CTTATGCTGAGATGAGTAAAGAGAGATGAGG--ATCATGTCTGTTAAGAGAAAGAG 2430
Qy 1356 GAGCCTCTGAGACCTTAAACAGGGTGGGAGGAGGCTGGGCGGAGAGACCAAGCCCA 1415
Db 2431 GAGCCTCTGAGACCTTAAACAGGGTGGGAGGAGGCTGGGCGGAGAGACCAAGCCCA 2489
Qy 1416 CTTTCACTCTCTTCCAGAGACGATCTCCCTGCGCACCATCCCATCATGGATGCTT 1475
Db 2490 CATTCCCTCTTCCAGAGACGATCTCCCTGCGCACCATCCCATCATGGATGCTT 2549
Qy 1476 GCTGGCGCTGCTGCTGAGTGTGAGTACATGAGAGCGGCGGCTGCTGCTGCTG 1535
Db 2550 GCTGGCGCTGCTGCTGAGTGTGAGTACATGAGAGCGGCGGCTGCTGCTGCTG 2609
Qy 1536 AGAAGAAGAGCTCAGTAAAGAGAGGAGTGAACAGTGGGCTGTGATTTCTTCTCCAC 1595
Db 2610 AGAAGAAGAGCTCAGTAAAGAGAGGAGTGAACAGTGGGCTGTGATTTCTTCTCCAC 2669
Qy 1596 TGGGGTTTCAAGCCAGGTAGAGTGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1655
Db 2670 TGGGGTTTCAAGCTCAGGTAGAGTGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2729
Qy 1656 CACTGAGGCTTACCCAGGCTGCGCTGTGTGTCAGACCTTCTTCTTGTAAAGAC 1715
Db 2730 CACTGAGGCTTACCCAGGCTGCGCTGTGTGTCAGACCTTCTTCTTGTAAAGAC 2788
Qy 1716 CTTGCAATGAGAGACATTTATTAACCTGATGATTTGATGATGAGGAGCTGATCC 1775
Db 2789 CTTGCAATGAGAGACATTTATTAACCTGATGATTTGATGATGAGGAGCTGATCC 2848
Qy 1776 AGTATATACAGCTCAGAGAGAGTCCCTGGCTTAAGAGACACTTAAGAGGAGTGGT 1835
Db 2849 AGTATATACAGCTCAGAGAGAGTCCCT--GCTGAGAGACACTTAAGAGGAGTGGT 2907
Qy 1836 CGAGGACCAACATCTGCTCTCTGTTTTCCTGATC--GCCCTGGCTCAGAGTCAAC 1893
Db 2908 CGAGGACCAACATCTGCTCTCTGTTTTCCTGATC--GCCCTGGCTCAGAGTCAAC 2967
Qy 1894 ATTTCTGAAATCTTCTGAGGCTCAAGACTAGAGAGTCTCTAGACCTCATAGGCCCT 1953
Db 2968 ATTTCTGAAATCTTCTGAGGCTCAAGACTAGAGAGTCTCTAGAGCTCATAGGCCCT 3027
Qy 1954 GCCACTTTCTGGGCTCTCAGAGACTTTTCTCCACAGTTCAAAAGAGAGAGTCA 2013
Db 3028 GCTACCTCTCTGCTCTCTCAGAGAGCTTTTCTCCGAGAGTAAAGAGAGAGTCA 3087
Qy 2014 CTTCTCAGGCTCAGTAAATGATGAGAGGCTGATCCTGAGATCCTTGGAGCTTGTGT 2073
Db 3088 CTTCTCAGGCTCAGTAAATGATGAGAGGCTGATCCTGAGATCCTTGGAGTATTTGTG 3147
1111 11 1111111111 1111111111

OY 2074 TTGGGAG-CCATGGGGGAGCTACCCACCACCAATTCCTCCTGTGGCACATCTCTGT 2132
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DB 3148 TTGGGAGCCCAATGGGGGAGCTACCCACCACCAATTCCTCCTTAGCCACATCTCTGT 3207
OY 2133 GGTCTTGACCAAGGTCGTGTTTTTTTCTACTTACGAGTACAGTCCCAAGGCTCTA 2192
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DB 3208 GGGATCTGACAGTTCGTGTTTTTCTTACCCAGGAGCCAAAGTCCCAAGGCTCTG 3267
OY 2193 ATGTCCTCTCAGGCTGTAAATGTGACACCCGGGGGCTGTATGTTGTGGTGTGTT 2252
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DB 3268 ATGTCTCTCAGGCTGTAAATGTGACACCCCTGGGAGGCTGATGTGTGGGTTGTT 3327
OY 2253 GAGGGACAGGGGACATAGCTGTGCTATAGAGTTCTTTCACCTCAATATATGAGCAT 2312
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DB 3328 G-GGGTAACAGTGAATATAGTGTGCTATGGGTTCTTGACTTGATATTCAGCAC 3386
OY 2313 GTGATGGGCTGTTTAAAGTGTACCCCTCCTGACTGATATGAAATTTGTTCATGATA 2372
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DB 3387 ATGATGGGCTGTCAAGGTGTACCCCTCCTGAGTATGAAATTTGTTCATGATA 3446
OY 2373 -TTTTCTGTAGTGAACAGCTGCCCTGTGTGGGACTGATGCAAGATTTGTTCATG 2431
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DB 3447 TTTTCTATAGTGTAGACAGCTGCTTGTGTGGGACTGAGAGCAATTTGTTCATG 3506
OY 2432 CCTTCCCTTTG 2442
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DB 3507 CCTTCCCTTTG 3517

RESULT 7
ID ABA18125 standard; DNA; 3098 BP.
XX ABA18125;

DT 23-JAN-2002 (first entry)

DE Human nervous system related polynucleotide SEQ ID NO 10456.

XX Human; nootropic; neuroprotective; cytosolic; dermatological; vlrucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulneryary;
KW antiParkinsonian; antisickling; antianaemic; antiarthritic; cancer;
KW antithematic; hepatotropic; cerebroprotective; antinflammatory;
KW antiallergic; antidiabetic; antilucer; anticonvulsant; antifungal;
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.

OS Homo sapiens.

XX WO200159063-A2.

PN 16-AUG-2001.

PE 17-JAN-2001; 2001WO-US01334.

XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
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PR 07-JUL-2000; 2000US-0216647.
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PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.

PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
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PR 20-OCT-2000; 2000US-0241808.
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PR 01-NOV-2000; 2000US-0246417.
PR 08-NOV-2000; 2000US-0246474.
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 PR 01-DEC-2000; 2000US-0250391.
 PR 01-DEC-2000; 2000US-0251160.
 PR 05-DEC-2000; 2000US-0251030.
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 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
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 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI: 2001-541565/60.
 XX
 PT Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating nervous system
 PT cancers and metastases -
 XX
 PS Disclosure: SEQ ID NO 10456; 1701tp + Sequence Listing: English.
 XX
 CC The invention relates to novel genes (ABA11004-ABA21534) and proteins
 CC (ABA14678-ABA18001) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal

CC and parasitic infections.

CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 3098 BP; 629 A; 858 C; 936 G; 675 T; 0 other;

Query Match 63.64; Score 1554; DB 22; Length 3098;
 Best Local Similarity 82.54; Pred. No. 0;

Matches 2047; Conservative 0; Mismatches 350; Indels 83; Gaps 20;

QY 1 TACTCCGAGTCTCCGGCTGTGGATCCACCCGAGGCGCGGACCCGACACCTTC
 Db 561 TCCCTCAGAGTCTCCGGATCCGAATCTACCCGAGGACGCGGACCCGACACCTTC
 QY 61 TACTCGGAGAGACCCCAAGGGCGCTTA-----CCAAATGCC 98
 Db 621 CACCCGAGAGTCTCCAGGCGCTTACCCAGGTTATTTTCAGTTAGGCCAAATGCC 680
 QY 99 CGCGGTTGGTCCGGGCGAGGCGAGGCTGGTGGCGGCGGCTGACCGAGGCGGTGGGCG 158
 Db 681 CGCGGTTGGGCGGCGGAGGCGGCGGCTGAGTGGCGGCGGCTGACTG-CGGGACCGGC 739
 QY 159 CAGGTTCTACACCTTCCTCAGTGATGTGGCGGACCTGGGGCTCCGAGGACGCTTC 218
 Db 740 TAGGCTCTACACCTTCCTCAGGATGATGTGGCTGCGCATGGGCGGCGGACGCTTC 799
 QY 219 TCCGCGGATATGAACAGTATGCTTACGATGCAAGATTTACCTCGCCCTGAACAGAGACC 278
 Db 800 TCCGCGGATATGACAGTATGCTTACGATGCAAGATTTACCTCGCCCTGAACAGAGACC 859
 QY 279 TGGGCTCTCGAGCGGCGGCGGACCTGCTGATGCTGACGCTTCTTCTGAGGCGG 338
 Db 860 TGGGCTCTCGAGCGGCGGCGGACCTGCTGATGCTGACGCTTCTTCTGAGGCGG 919
 QY 339 CCAATGTGCTGACCAAGAGAGAGACCTTACCTGAGGCGGACGCTGAGTGGCTCCACA 398
 Db 920 AGGAATATGACAGAGAGATTCAGACCTTACCTGAGGCGGCGGCTGAGTGGCTCCACA 979
 QY 399 GATACCTGAGAGAGAGAGAGAGATGCTGAGGCGGCGGCTGAGTGGCTGAGGCGGCG 458
 Db 980 GATACCTGAGAGAGAGAGAGAGATGCTGAGGCGGCGGCTGAGTGGCTGAGGCGGCG 1038
 QY 459 CTCCTGATCTCTGATGACCTCTCAGCTGCGCTGACACAGAGAGAGAGAGAGAGAG 518
 Db 1039 CTCCTGATCTCTGATGACCTCTCAGCTGCGCTGACACAGAGAGAGAGAGAGAGAG 1098
 QY 519 ACCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 578
 Db 1099 CCCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1158
 QY 579 CAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 638
 Db 1159 GAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1218
 QY 639 ATGAAGTCTGAGAGAGATGAGAGAGAGAGAGATGATGATGATGATGATGATGATG 698
 Db 1219 ATGAATCTGAGAGAGATGAGAGAGAGAGAGATGATGATGATGATGATGATGATG 1277
 QY 699 TTTGA-CCCCACACAGCTTTGGACAGAGACTTTTCCCTCAGGCGCTTCTGCTGCT 757
 Db 1278 TTTGAGCCCTCCACACAGCTTTGGGCGGCGGCTTCTGCAAGTTCTTCTGCTGCT 1337
 QY 758 CACACTCATATGTGTGGGGGTCTGATCTCAGTCTCTGATGCTTGGCTCTCCTCACTA 817
 Db 1338 CACACTCATATGTGTGGGGGTCTGATCTCAGTCTCTGATGCTTGGCTCTCCTCACTA 1387
 QY 818 GGTGAGACCGAGAGCTGCTGCTCCCGCTCAGAGACTGAGACTTTCAGAGATATAGA 877
 Db 1388 GGTGAGGCGAGAGCTGCTGCTCCCGCTCAGAGACTGAGACTTTCAGAGATATAGA 1446
 QY 878 GATATCTCAGAGCTCCGCTGCTCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 937
 Db 1446 GATATCTCAGAGCTCCGCTGCTCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT

Db 1447 GATTTCACAGTGTCTGTGTCACAGGCTGTGTGTTCTGTGCTCCCTCCACACC 1506
 QY 938 CAGGTATCTGTTCACTTTAGATGTGCATACATCCAGATGTTGGATGTTCCCATAG 997
 Db 1507 CAGGTATCTGTTCACTTTAGATGTGCATACATCCAGATGTTGGATGTTCCCATAG 1554
 QY 998 AGATGCAAGTGTGATTTTCTGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1057
 Db 1565 GAGTCAAGTGTGATTTTCTGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1621
 QY 1058 CCCACGACCCCTGTTGATATGAGGACCCCTGAGGCTGTGGGCTGTGGCTCTTAC 1117
 Db 1622 CCCACGACCCCTGTTGATATGAGGACCCCTGAGGCTGTGGGCTGTGGCTCTTAC 1661
 QY 1118 CTGCGGAGATCAATCTGACCTGTGACAGGGGATGGGAGACCCAGACAGCTGAGC 1177
 Db 1682 CTGCGGAGATCAATCTGACCTGTGACAGGGGATGGGAGACCCAGACAGCTGAGC 1741
 QY 1178 TCGTGGAGACGCGCTGACGGGGATGSAACCTCCAGAAAGTGGGCTGTGGTGTGC 1237
 Db 1742 TCGTGGAGACGCGCTGACGGGGATGSAACCTCCAGAAAGTGGGCTGTGGTGTGC 1801
 QY 1238 CTCTGAGAGAGACAGATACAGCTGATGTGACGATGAGGGGCTGTGGGAGCC 1297
 Db 1802 CTCTGAGAGAGACAGATACAGCTGATGTGACGATGAGGGGCTGTGGGAGCC 1861
 QY 1298 TCATGCTGAGATGAGCTAAGGAGGAGAT-----GGAGGATCAGT 1339
 Db 1862 TCATGCTGAGATGAGCTAAGGAGGAGATGGGTAAGAGGGGAGGAGGCTGATCTT 1921
 QY 1340 CTGTTAGGGAAGAGAGAGGCTCTCTGAAGACCTTTAAGGGTGTGGTGGAGGCTG 1399
 Db 1922 TTTCTAGGGAAGAGAGAGGCTCTCTGAAGACCTTTAAGGGTGTGGTGGAGGCTG 1981
 QY 1400 GGGTCAAGACCCCTGACCTTACCTCTTCCAGAGAGCTCTTCCCTGCCACATCC 1459
 Db 1982 AGATCAAGGAGGCTGACCTTCCCTTCCAGAGAGCTCTTCCCTGCCACATCC 2041
 QY 1460 CATCATGGGATGCTGCTGGCTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1519
 Db 2042 CATCATGGGATGCTGCTGGCTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2101
 QY 1520 CGCTGCTGTGCTGTGGAGAAAGAGCTGAGTAAAGAGGGGTGACATGGGGCTG 1579
 Db 2102 CGCTGCTGTGCTGTGGAGAAAGAGCTGAGTAAAGAGGGGTGAGAGTGGCTG 2160
 QY 1580 AGTTTCTGTCCACTGAGGGGTTTCAAGCCAGAGTAAAGTGTGCTGTGCTGTTAC 1639
 Db 2161 AGTTTCTGTCCACTGAGGGGTTTCAAGCCAGAGTAAAGTGTGCTGTGCTGTTAC 2220
 QY 1640 TGGAGAGACCATCCACATCATATGGGCTTACCAGCTGTGGCTGTGCCAGCCTT 1699
 Db 2221 TGGAGAGACCATCCACATCATATGGGCTTACCAGCTGTGGCTGTGCCAGCCTT 2280
 QY 1700 CTCTTTTGAAGACCTGTGACATGATGAAGAGACATTTATTAACCTGTGATTTAGTG 1759
 Db 2281 CTCTTTTGAAGACCTGTGACATGATGAAGAGACATTTATTAACCTGTGATTTAGTG 2340
 QY 1760 ATG--GGAGCTGATCCCACTAATCAAGGTCA--GGAGAGTCCCTGTGAAGACAGA 1816
 Db 2341 GTGATGGGACTGATCCCACTAATCAAGGTCAAGGAGGAGGAGTCCCTGTGATGACGA 2400
 QY 1817 CTTTGAAGGAGGACATGTTGGAGAGCCACATGCTTCTCTGTTTCTCTGATC--GC 1874
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 QY 1875 CCGTGGTCTGAGTCAACATTTCTGAAATCTTCTGAGGGTCAAGACTAGAGGTTCC 1934
 Db 2461 CCGTGGTCTGAGTCAACATTTCTGAAATCTTCTGAGGGTCAAGACTAGAGGTTCC 2520
 QY 1935 TCTTGAAGGAGGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1994
 Db 2521 TCTTGAAGGAGGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580

QY 1995 ATTGAAGAGAGGAGAGTACTCTCAGCTGCAATGATGAGAGGAGGCTGATCCCTGA 2054
 Db 2581 ATGGAAGAGAGGAGAGTACTCTCAGCTGCAATGATGAGAGGAGGCTGATCCCTGA 2639
 QY 2055 GATCTTGGAGATCTTGTGTTGGAGCC--ATGGGAGAGTCAACCCACCAATTCCTC 2113
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 QY 2114 CTCTGCGACCATCTCTGCTGTGCTGACAGGCTGTGTTGTTGTTGTTGTTGTTG 2173
 Db 2700 -----TACCCATCTCTGTGGCTCTGACAGCTCTGTTTGTCTACCCATCACT 2753
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 ID AAS40421 standard; DNA; 3098 BP.
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 AC AAS40421;
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 DT 17-DEC-2001 (first entry)
 XX
 DE DNA encoding human prostate cancer antigen, Seq ID No 573.
 XX
 KW Human; prostate cancer antigen; cytosolic; uropathic; diagnostic;
 KW reproductive system; chromosomal marker; forensic; urinary disorder;
 KW chronic nephritis; blood-related disorder; thrombosis; ds.
 XX
 OS Homo sapiens.
 PN WO20015316-A2.
 PD 02-AUG-2001.
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 PF 17-JAN-2001; 2001WO-US01328.
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 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
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 PR 18-APR-2000; 2000US-0198123.
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 PR 07-JUN-2000; 2000US-0209467.
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 PR 17-NOV-2000; 2000US-0249265.
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 PR 01-DEC-2000; 2000US-0250160.
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 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
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 PR 08-DEC-2000; 2000US-0251989.
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 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX
 PT Rosen CA, Barash SC, Ruben SM;
 DR WPI; 2001-451929/48.
 XX
 XX
 PT Isolated polypeptide for treating, preventing and/or prognosing
 PT disorders related to the reproductive system including prostate cancer
 PT and also for testing and detection e.g. diagnosis -
 XX
 PS Disclosure; SEQ ID No 573; 546pp; English.
 XX
 CC The invention relates to novel isolated human prostate cancer antigen
 CC polynucleotides (I) and polypeptides (II). (I) and (II) are useful for
 CC preventing, treating or ameliorating a medical condition when
 CC administered. (I), (II) and the antibody to (II) are useful for treating,
 CC preventing and/or prognosing disorders related to the reproductive
 CC system including prostate cancers; urinary disorders e.g. chronic
 CC nephritis; and blood-related disorders e.g. thrombosis. (II) can be used
 CC for testing and detection e.g. as a chromosomal marker and in forensics.
 CC (I) and the anti-(II) antibody can be used in testing and detection in
 CC immunoassays. AAS40061-AAS40775 represent the human prostate cancer
 CC antigen coding sequences, and related PCR primers and sequences of the
 CC invention. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at: ftp.wipo.int/pub/published_pct_sequences.

xx Sequence 3098 BP; 629 A; 858 C; 936 G; 675 T; 0 other:
SQ
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Best Local Similarity 82.5%; Pred. No. 0;
Matches 2047; Conservative 0; Mismatches 350; Indels 83; Gaps 20:
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DB 621 CACCCGGGAGAGTCCCAAGGCCCTTTTACCCAGGTTCAATTTTAGGCTTAATCCC 680
QY 99 CCGGAGGTGCTCCGGCGAGCGAGGCTGCGTGGCGGGGCTACCGAGGAGGGGTGGGG 158
DB 661 CGCGGGTTGGCGGGGAGGGGGGGGGCTAGCTGGCGGGGGCTGACTG-CGGGACCGGG 739
QY 159 CAGTTCTCACACCTCCAGTGATGATTTGGCTCGACCTGGGGTCCGACGAGCCTCC 218
DB 740 TAGGGTCTCACACCTCCAGGGAATGAATGGCTCGACATGGGGCCCGAGCGAGCGCTCC 799
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DB 1039 CTTCCTATCTCTGTAGATCTTGTGGGATGCGCTCGCACAAGTGTGGAGAAAGTGA 1098
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DB 1099 CCCAATGCTAGGATATCGCCCTCCCTCTAGTCTCTAGTAGAAGAAATTTCTCTGGCTTC 1158
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QY 758 CACACTCATGTGTGGGGGTGTGACTCAGCTCTGAGTCCCTTGGCTCTCAGCTCA 817
DB 1338 CACACTCATGTGTGGGGGTGTGACTCAGCTCTGAGTCC-----AGTCCCTGGGCTCCACCTTA 1387
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QY 998 AGATGCAAAAGTCTTGAAATTTTCTGACTCTCTCTTTCACAGACCCCGGAGACAGAGTGA 1057
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DB 1622 CCCACACCCCATTTCTGTACCATGAGGCCACCTGAGGTGCTGGGCCCTTGTCTTAC 1681
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QY 1700 CTCTTTTGAAGCAGCTGTGACAAATGAAGAGAGATTTTATCTTGTATGTGTATG 1759
DB 2281 CTCTTTTGAAGCAGCTGTGACAAATGAAGAGAGATTTTATCTTGTATGTGTATG 2340
QY 1760 ATG--GGGAGCTGATCCGATATACAGAGTCA--GGAGAGGTTCCCTGGAAGACAGA 1816
DB 2341 GTGATGGAGCTGATCCGAGAGTCAAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
QY 1817 CTTTGAAGGAGGAGT 1874
DB 2401 CTTTGAAGGAGGAGT 2460
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DB 2461 CTTGAGTCTGAGTCAACATTTCTGGAAGCTTCTGAGAGGCTCAAGAGTGTGAGAGTCC 2520
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QY 1995 ATTGAAAGAGAGGAGCTACTCTGAGGCTGACAGTAAAGTATGAGAGAGGCTGATCCCTGA 2054
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 PR 05-DEC-2000; 2000US-0251719.
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 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI; 2001-465570/50.
 XX
 PT Isolated nucleic acid molecule encoding a reproductive system antigen
 XX is used in preventing, treating or ameliorating a medical condition -
 PS Disclosure: SEQ ID NO 6712; 1297PP + Sequence Listing; English.
 XX
 CC The present invention provides the protein and coding sequences of a
 CC number of human reproductive system related antigens. These can be used
 CC in the prevention and treatment of reproductive system disorders,
 CC including cancer. The present sequence is a genomic sequence encoding a
 CC protein of the invention.
 XX
 SQ Sequence 3098 BP; 629 A; 858 C; 936 G; 675 T; 0 other;
 QY
 Best Match 63.6%; Score 1554; DB 22; Length 3098;
 Best Local Similarity 82.5%; Pred. No. 0;
 Matches 2047; Conservative 0; Mismatches 350; Indels 83; Gaps 20;
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Qy 1760 ATG--GGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1816
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RESULT 10
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AC AAK86871;
DT 07-NOV-2001 (first entry)
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DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41683.
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytosolic; gene therapy; vaccine; metastasis; ds.
OS Homo sapiens.
PN WO200157182-A2.
PD 09-AUG-2001.
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PF 17-JAN-2001; 2001MO-US01354.
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PR 31-JAN-2000; 2000US-0179065.
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PR	20-OCT-2000	2000US-0241826
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PR	08-NOV-2000	2000US-0244674
PR	08-NOV-2000	2000US-0244675
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PR	08-NOV-2000	2000US-0245609
PR	08-NOV-2000	2000US-0245610
PR	08-NOV-2000	2000US-0245611
PR	08-NOV-2000	2000US-0245613
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PR	17-NOV-2000	2000US-0249209
PR	17-NOV-2000	2000US-0249210
PR	17-NOV-2000	2000US-0249211
PR	17-NOV-2000	2000US-0249212

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	PR	17-NOV-2000;	2000US-0249214.
	PR	17-NOV-2000;	2000US-0249215.
	PR	17-NOV-2000;	2000US-0249216.
	PR	17-NOV-2000;	2000US-0249217.
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	PR	17-NOV-2000;	2000US-0249219.
	PR	17-NOV-2000;	2000US-0249224.
	PR	17-NOV-2000;	2000US-0249245.
	PR	17-NOV-2000;	2000US-0249264.
	PR	17-NOV-2000;	2000US-0249265.
	PR	17-NOV-2000;	2000US-0249297.
	PR	17-NOV-2000;	2000US-0249299.
	PR	01-DEC-2000;	2000US-0249300.
	PR	01-DEC-2000;	2000US-0250160.
	PR	05-DEC-2000;	2000US-0250391.
	PR	05-DEC-2000;	2000US-0251030.
	PR	05-DEC-2000;	2000US-0251988.
	PR	05-DEC-2000;	2000US-0256719.
	PR	06-DEC-2000;	2000US-0251479.
	PR	08-DEC-2000;	2000US-0251856.
	PR	08-DEC-2000;	2000US-0251866.
	PR	08-DEC-2000;	2000US-0251869.
	PR	08-DEC-2000;	2000US-0251989.
	PR	08-DEC-2000;	2000US-0251990.
	PR	11-DEC-2000;	2000US-0254097.
	PR	05-JAN-2001;	2001US-0259678.
PA	(HUMA -)	HUMAN GENOME SCI INC.	
PX	Rosen CA,	Barash SC,	Ruben SM;
PI	WPI:	2001-483426/52.	
DR	Nucleic acids encoding human immune/hematopoietic antigen polypeptides,		
PT	Nucleic acid preventing, diagnosing and/or treating cancers and		
PT	metastasis -		
PS	Disclosure; SEQ ID NO 41683; 3071pp + Sequence Listing; English.		
XX	AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)		
CC	amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic		
CC	activity, and can be used in gene therapy and vaccine production. (I)		
CC	proteins and polynucleotides may be used in the prevention, diagnosis and		
CC	treatment of diseases associated with inappropriate (I) expression. For		
CC	example, they may be used to treat disorders associated with decreased		
CC	expression by rectifying mutations or deletions in a patient's genome		
CC	that affect the activity of (I) by expressing inactive proteins or to		
CC	supplement the patients own production of (I). Additionally, (I)		
CC	polynucleotides may be used to produce the secreted (I), by inserting the		
CC	nucleic acids into a host cell and culturing the cell to express the		
CC	protein. (I) proteins and polynucleotides may be used to prevent,		
CC	diagnose and treat immune/hematopoietic-related diseases, especially		
CC	cancers and cancer metastases of haematopoietic-derived cells. AAK64703		
CC	to AAK87694 represent human immune/hematopoietic antigen genomic		
CC	sequences from the present invention. AAK54942 to AAK54950 and AAM82169		
CC	represent sequences used in the exemplification of the present invention.		
XX	Sequence 3098 BP; 629 A; 858 C; 936 G; 675 T; 0 other:		
SQ			
	Query Match	63.6%;	Score 1554; DB 22; Length 3098;
	Best Local Similarity	82.5%;	Pred. No. 0;
	Matches 2047; Conservative	0;	Mismatches 350; Indels 83; Gaps 20
OY	I TACGCCGAGTCCTCGGGATCCACCAGCAGCCGCGGAGCCGCACAGACCTC 60		
Dd	TCCCTCAAGTCTCCGATCCGAATCTACCCGAGGACGAGGACCCGACAGACTTC 620		
OY	61 TACCTGGAGAACCCCAAGCGCCTTTA-----CCAATGCC 98		
Dd	621 CACCGGAGAAGTCCCGAGCGCCTTACCCAGGTGTAATTTCAGTTTAGGCCCAAATTC 680		
OY	CGCGGGTGAGTCCGCGGAGGCGAGGCTCGTGGGGGGGGGCTGACGAGAGGGGTGGGCG 158		

OY 2286 TTCTTTCAGCTTCATGATTTGAGCATGTGATGGCTGTTTAAATGTCACCCCTCAGTG 2345
 CC ||||||| ||| ||||||| ||||| ||| ||| ||| ||| |||
 CC 2874 TTCTTTCAGCTTCATGATTTGAGCATGAAATGGCTATTAGATGTTACTCTCAGTG 2933
 CC ||||||| ||| ||||||| ||||| ||| ||| ||| ||| |||
 OY 2346 TGACTGATGATTTGTTTATATATATTTT -TCTGAGTGTAACAGCTGCCCTGTG 2404
 CC ||||||| ||| ||||||| ||||| ||| ||| ||| ||| |||
 Db 2934 TGACTGATGAGAAATTTGTTATATATATTTTCTATAGTGAGACAGCTTCTTGTTG 2993
 CC ||||||| ||| ||||||| ||||| ||| ||| ||| ||| |||
 OY 2405 GGGACTGAGTGGCAAGATT 2424
 CC ||||||| ||| ||||||| ||||| ||| ||| ||| ||| |||
 Db 2994 GGGACTGAGAAAGCAAGATT 3013
 CC ||||||| ||| ||||||| ||||| ||| ||| ||| ||| |||
 RESULT 11
 ABA83122
 ID ABA83122 standard; DNA: 4316 BP.
 AC ABA83122;
 XX
 XX 08-FEB-2002 (first entry)
 DT
 DE HLA-Cw ovarian tumour marker gene, SEQ ID NO:81.
 XX
 KW Ovarian tumour marker gene; human; overexpression; upregulation;
 KW epithelial tumour; cancer; diagnosis; prognosis; disease monitoring;
 KW identification; serous cystadenoma; borderline serous tumour;
 KW mucinous cystadenocarcinoma; mucinous cystadenocarcinoma;
 KW mucinous cystadenoma; borderline mucinous tumour; endometrioid carcinoma;
 KW undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma;
 KW adenofibroma; Brenner tumour; serial analysis of gene expression; SAGE;
 KW immune response pathway; cell proliferation regulation; protein folding;
 KW membrane localised; secreted; therapeutic target; cytostatic;
 KW gene therapy; vaccine; ds.
 KW
 OS Homo sapiens.
 XX
 XX WO200175177-A2.
 PM
 XX 11-OCT-2001.
 PD
 XX 03-APR-2001; 2001WO-US10947.
 PF
 XX 03-APR-2000; 2000US-194336P.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Morin PJ, Sherman-Baust CA, Pizer ES, Hough CD;
 PI
 XX MPI: 2001-626450/72.
 DR
 XX P-PSDB: ABB50296.
 DR
 XX
 PT Detecting and identifying ovarian tumor, identifying increased risk for
 PT developing ovarian cancer, and determining effectiveness of ovarian
 PT cancer treatment, by measuring expression level of ovarian tumor marker
 PT gene -
 PS
 XX Claim 23: Page 124-126; 140pp; English.
 XX
 CC The invention relates to methods for diagnosing and prognosing ovarian
 CC tumors in an individual via the detection and measurement of the
 CC expression of ovarian tumour marker genes (ABA83081-ABA83122, ABA83180,
 CC ABA83182 and ABA83184) or segments thereof (ABA83123-ABA83169, ABA83179,
 CC ABA83181 and ABA83183). The methods of the invention are useful for
 CC detecting an ovarian tumour in a patient, for identifying an individual
 CC at increased risk for developing ovarian cancer, in prognostic tests for
 CC assessing the relative severity of ovarian cancer, in tests for
 CC monitoring a patient in remission from ovarian cancer and in tests for
 CC monitoring disease status in a patient being treated for ovarian cancer.
 CC The methods can additionally be used to identify a particular tumour as
 CC being an ovarian tumour (i.e., an epithelial ovarian tumour selected from
 CC serous cystadenoma, borderline serous tumour, serous cystadenocarcinoma,
 CC mucinous cystadenoma, borderline mucinous tumour, mucinous
 CC cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma,

CC clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner
 CC tumour. The ovarian tumour marker genes of the invention were identified
 CC using SAGE (serial analysis of gene expression) and were found to be
 CC overexpressed in a broad variety of ovarian epithelial tumour cells
 CC relative to normal ovarian epithelial cells. The marker genes are
 CC implicated in immune response pathways, in the regulation of cell
 CC proliferation and in protein folding, and many of these are membrane-
 CC localised or secreted. In addition to their use as diagnostic and
 CC prognostic markers, the ovarian tumour marker genes or their encoded
 CC proteins may be used as therapeutic targets for the treatment and
 CC prevention of ovarian cancer. Sequences ABA83081-ABA83122, ABA83180,
 CC ABA83182 and ABA83184 represent the ovarian tumour marker genes of
 CC the invention.
 CC
 XX
 SQ Sequence 4316 BP; 1000 A; 1090 C; 1292 G; 934 T; 0 other;
 Query Match 63.5%; Score 1551.6; DB 22; Length 4316;
 Best Local Similarity 82.7%; Pred. No. 0;
 Matches 2052; Conservative 0; Mismatches 344; Indels 84; Gaps 21;
 OY 1 TACTCCCGAGTCTCCGGGCTGGATCCACCCCGGCGGACCCCGCAGACCTTC 60
 Db 1377 TCCCCCGAGTCTCCGGGCTGGATCCGAAATCTACCCGAGGACGC -GACCCCGCAGACCTTC 1435
 OY 61 TACTGGAGAACCCCAAGGCGCCTTTA-----CCAAATCCC 98
 Db 1436 CACCCGGAGAGTCCCAAGGCGCCTTTACGAGGTTTATTTAGTTAGGCCAAATCCC 1495
 OY 99 CGCGGTGGGTCCGGCGGAGGCGGAGGCTCGGTGGCGGGGCTGCAGCCAGGGGTGGGCG 158
 Db 1496 CGCGGTGGGTGGCGGAGGCGGAGGCTCGGTGGCGGGGCTGCAGCTG -CGGGACCGCG 1554
 OY 159 CAGGTTCACACCCCTTCAGTGTGATTTGTCGACACCTCGGGGCTCGACGAGCCTCC 218
 Db 1555 TAGGCTTCACACCCCTTCAGGATGATGATGCTGCGACATGGGGCCGACGAGCCTCC 1614
 OY 219 TCCGCGGATGAGAGTATCTCAGTATGCGAAGATTACCTCCGCCCTGAAAGAGACC 278
 Db 1615 TCCGCGGATGAGAGTATCTCAGTATGCGAAGATTACCTCCGCCCTGAAAGAGACC 1674
 OY 279 TGGGCTCTGGAGCGGAGGAGACCTCGGCTCAGATCTCCAAGCGCAAGTGTAGGCGG 338
 Db 1675 TGGGCTCTGGAGCGGAGGAGACCTCGGCTCAGATCTCCAAGCGCAAGTGTAGGCGG 1734
 OY 339 CCAATGTGGCTGAAACAAGAGAGCTTACCTGAGGGCAGCTGGCTGCTCCACA 398
 Db 1735 AGGAATATGCAAGAGAGTTCAGGACTACCTGAGGGCGAGTGGCTGCTCCACA 1794
 OY 399 GATACCTGGAGAACGGGAAGAGATGCTGCAGCGCGGGGATACCGAGGGGCGCAT 458
 Db 1795 GATACCTGGAGAACGGGAAGAGATGCTGCAGCGCGGGGATACCGAGGGGCGCAT 463
 OY 459 CTCCTCGATTCCTGTAGACTCTCAGCTGAGCTGAGCAGACAGAGAGGAAATAGG 518
 Db 1854 CTCCTCGATTCCTGTAGACTCTCAGCTGAGCTGAGCAGACAGAGTGGAGAAATAGG 513
 OY 519 ACCAAGCTGAGATATCGCCCTCTCTGCTGTGAGGAGAGGAATCTCTGGGTTTC 578
 Db 1914 CCAATGTGATGATATCGCCCTCTCTGCTGTGAGGAGAGGAATCTCTGGGTTTC 1973
 OY 579 CAGATCTCTGACAGAGTGTCTGAGGGCGCGCTCTGCTCTGGAGCAATTAAGG 638
 Db 1974 GAGATCTCTGACAGAGTGTCTGAGGGCGCGCTCTGCTCTGGAGCAATTAAGG 2033
 OY 639 ATGAGCTCTGAGAGGAGTGTGAGGAGAGCAATCTCGGAAGATGATGAGGGTTCC 698
 Db 2034 ATGAAATCTGAGAGGAGTGTGAGGAGAGCAATCTCGGAATGATGAGGGTTCC 2092
 OY 699 TTGGA-CCCAACAGAGCTTGGACACAGACTTTTCCCTCAGGCTTGTCTGGCT 757
 Db 2093 TTGAGCCCTCCACAGAGCTTGGGCGCGTGAATTTTCTCTCAAGTTTGTCTGCT 2152
 OY 758 CACACTCAATGTGTGTGGGGGTCTGATTCAGCTCTCTGATGCTCCTTGGCTCCACTCA 817

Db 2153 CACATCAATGTGTTGGGGTCTGATTCC-----AGTCCCTCGGCTCCACCTTA 2202
 QY 818 GGTCAAGAACCGAGAGTCCCTGCTCCCGCTCAGAGACTTGAACCTTTCCAGAGATAGGA 877
 Db 2203 GGTCAAGAACCGAGAGTCCCTGCTCCCGCTCAGAGACTTGAACCTTTCCAGAGATAGGA 2261
 QY 878 GATTATCCAGAGTCCCGCTGCTCAGAGTGGTGTCTGAGTCTGAGTCCCTCCACCC 937
 Db 2262 GATTATCCAGAGTCCCGCTGCTCAGAGTGGTGTCTGAGTCTGAGTCCCTCCACCC 2321
 QY 938 CAGGATCTGCTGATCTTATGAGATGCTCAGATCCAGAGTCTGCTGAGTCTGAGTCC 997
 Db 2322 CAGGATCTGCTGATCTTATGAGATGCTCAGATCCAGAGTCTGCTGAGTCTGAGTCC 2379
 QY 998 AGATCAAGTCTGATCTTATGAGATGCTCAGATCCAGAGTCTGCTGAGTCTGAGTCC 1057
 Db 2380 AGATCAAGTCTGATCTTATGAGATGCTCAGATCCAGAGTCTGCTGAGTCTGAGTCC 2436
 QY 1058 CCGACACCTGCTGATCTTATGAGATGCTCAGAGTCTGCTGAGTCTGAGTCTGAGTCC 1117
 Db 2437 CCGACACCTGCTGATCTTATGAGATGCTCAGAGTCTGCTGAGTCTGAGTCTGAGTCC 2496
 QY 1118 CTGCGAGATCTGATCTTATGAGATGCTCAGAGTGGATGGAGACACAGAGTCTGAGTCC 1177
 Db 2497 CTGCGAGATCTGATCTTATGAGATGCTCAGAGTGGATGGAGACACAGAGTCTGAGTCC 2556
 QY 1178 TCGTGAAGACACGAGTCTGAGAGGATGGAGTCTTCCAGAGTGGATGGAGTCTGAGTCC 1237
 Db 2557 TCGTGAAGACACGAGTCTGAGAGGATGGAGTCTTCCAGAGTGGATGGAGTCTGAGTCC 2616
 QY 1238 CTTCGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1297
 Db 2617 CTTCGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2676
 QY 1298 TCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1339
 Db 2677 TCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2736
 QY 1340 CTGTTAGGAG 1399
 Db 2737 CTGTTAGGAG 2796
 QY 1400 GGGTCAG 1459
 Db 2797 AGATCAG 2856
 QY 1460 CATCATGGGATCTGTTGCTGAGCTGTTGCTGAGCTGATGATGATGATGATGATGATG 1519
 Db 2857 CATCATGGGATCTGTTGCTGAGCTGTTGCTGAGCTGATGATGATGATGATGATGATG 2916
 QY 1520 GCGTCTGCTGCTGAG 1579
 Db 2917 GCGTCTGCTGCTGAG 2975
 QY 1580 AGTTTCTGTTGCTGAG 1639
 Db 2976 AGTTTCTGTTGCTGAG 3035
 QY 1640 TGGAG 1699
 Db 3036 TGGAG 3095
 QY 1700 CTCTTTTAAAGACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1759
 Db 3096 CTCTTTTAAAGACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3155
 QY 1760 ATG--GGGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1816
 Db 3156 GTGATGAG 3215
 QY 1817 CCTTAG 3274
 Db 3215 CCTTAG 3274

Db 3216 CCTCAG 3275
 QY 1875 CTTGGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1934
 Db 3276 CTTGGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3335
 QY 1935 TCTAG 1994
 Db 3336 TCTAG 3395
 QY 1995 ATTGAAG 2054
 Db 3396 ATTGAAG 3454
 QY 2055 GATCTGAG 2113
 Db 3455 GATCTGAG 3514
 QY 2114 CTCTGAG 2173
 Db 3515 CTCTGAG 3568
 QY 2174 GACAGTGGCCAG 2228
 Db 3569 GACAGTGGCCAG 3628
 QY 2229 GGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2285
 Db 3629 GGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3688
 QY 2286 TTTCTTGAAG 2345
 Db 3689 TTTCTTGAAG 3748
 QY 2346 TGAAGTGAAG 2404
 Db 3749 TGAAGTGAAG 3808
 QY 2405 GGGAGTGAAG 2464
 Db 3809 GGGAGTGAAG 3868

RESULT 12
 ID ABN97218 standard; DNA; 4316 BP.
 XX
 AC ABN97218;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE Gene #3716 used to diagnose liver cancer.
 XX
 KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
 KW metastatic liver tumor; cytosolic; expression profile; disease state;
 KW disease progression; drug toxicity; drug efficacy; drug metabolism.
 XX
 OS Homo sapiens.
 XX
 PN W0200229103-A2.
 XX
 PD 11-APR-2002.
 XX
 XX 02-OCT-2001; 2001WO-US30589.
 XX
 XX 02-OCT-2000; 2000US-237054P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Horne D, Alvares C, Beres-Da-Silva S, Vockley JG;
 XX
 DR WPI; 2002-426119/45.
 XX

PT Diagnosing and detecting the progression of liver cancer,
PT hepatocellular carcinoma or metastatic liver tumor in a patient,
PT involves detecting the level of expression of two or more genes in a
PT liver tissue sample
XX
XX Claim 1: SEQ ID NO 3716; 298bp; English.
XX
CC The invention relates to a novel method for diagnosing and detecting the
CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC tumour in a patient, and differentiating metastatic liver cancer from
CC hepatocellular carcinoma in a patient, involving detecting the level of
CC expression of two or more genes represented in ABN93503-ABN97455 in a
CC tissue sample. The method of the invention has hepatotropic, and
CC cytosolic activity. The method is useful for diagnosing and detecting
CC the progression of liver cancer, hepatocellular carcinoma and metastatic
CC liver carcinoma in a patient. The method is useful for identifying
CC expression profiles which serve as useful diagnostic markers as well as
CC markers that can be used to monitor disease states, disease progression,
CC drug toxicity, drug efficacy and drug metabolism.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX

Sequence 4316 Bp: 1000 A; 1090 C; 1292 G; 934 T; 0 other:

Query Match 63.5%; Score 1551.6; DB 24; Length 4316;

Best Local Similarity 82.7%; Pred. No. 0;

Matches 2052; Conservative 0; Mismatches 344; Indels 84; Gaps 21;

OY 1 TACTCCGAGTCTCCGGGTCTGGATCCACCCGAGGCGCGCGGACCCGACGACCTTC 60
DB 1377 TCCCCCGAGTCTCCGGATCCGAATCTACCCCGAGGCGAGC-GGACCGCGCGACGCTC 1435
OY 61 TACCTGGGAGAACCCCAAGGCGCTTTA-----CCAAATCCC 98
DB 1436 CACCCGAGAGAGTCCAGCGCGCTTACCAGATTCATTTTACGTTTACGCAAAATCCC 1495
OY 99 CCGCGGTGGGTCCGGCGAGGCGAGGCGGTCGGTGGGCGGGGCGACCGAGGGTGGGCG 158
DB 1496 CCGGGTTGGGGGGGGGGGGGGGGCTAGCTGGGGGGGCTGACTG-CGGGGACCGGCG 1554
OY 159 CAGGTCTCAACACCTCTCAGTGTGATTTGGCTGCAGCTGGGGGTCCGACGAGCGCTTC 218
DB 1555 TAGGCTCAACACCTCTCAGGGAATGATGGCTGCACATGGGGCGCGACGCGCTTC 1614
OY 219 TCCGCGGGTATGACAGTATGCTTACGATGGCAGGATTAACCTCCGCTGAACGAGACC 278
DB 1615 TCCGCGGGTATGACAGCAGCGCTACGAGCGGCAAGGATTAACATCTCCGTAACGAGACC 1674
OY 279 TGGGCTCCTGGACCGAGCGACACTCGGCTCAGATCTCCAGCGCAAGTGTAGGCGG 338
DB 1675 TGGGCTCCTGGACCGCGGGGACACCGTGGCTCAGATCCACCGCGCTTCTAGAGGAG 1734
OY 339 CCAATGTGCTGAACAAAGAGAGCCTACCTGAGGGGACAGCTGGAGTGGCTCCACA 398
DB 1735 AGGAATATGCAAGAGATTGAGAGCTACCTGAGGGCGAGTCTCGTAGTTGCTCCGGA 1794
OY 399 GATATCTGGGAACGGGAAGAGATGTGACGGCGGGGTACCAAGGGGAGGAGGGGCG 458
DB 1795 GATATCTGGGAATGGGAAGAGAGCTACGAGCGGAGGTACCAAGGGGAGGAGGCGAT 1853
OY 459 CTCCTGATCTCCTGTAGACCTCTCAGCCTTGCCCTAGCAGCAAGAGAGAGAAAAATGG 518
DB 1854 CTTCCTATCTCTCTGTATCTCTTGGGATGGCTGCGACAAGGTTGGGAGAAAGTGG 1913
OY 519 ACCAACAATGATATGCCCCCTCCCTGTGCTGAGGAGAGAGATCTCTCGGGTTTC 578
DB 1914 CCAATCTAGGATATGCCCCCTCCCTGTAGTCTGAGTAGAAGAACTTCTGGCTTTC 1973
OY 579 CAGATCTGTAACGAGAGATGATTTGAGGGCGCGCTCTCTCTGAGCAATTAAGGG 638
DB 1974 GAGATCCGGTACAGAGAGTACTGTGAGAGTCCGCCCTGCTCTGTGGACAAATTAAGG 2033

OY 639 ATGAGTCTCTGAGGAGTGGAGGAGAACAAATCCCTGGAAAGTATCAGGGTTCCC 698
DB 2034 ATGAATCTCTGAGGGAATGGA-GGGAAGACATCTCCCTGGAAATACGATCCGGGTCGCC 2092
OY 699 TTTGA-CCCCACAGACACCTTGGCACCAGGACTTTTCCCTCAGGCTTGTCTGCTCT 757
DB 2093 TTTGAGCCCTTCAACACACTTGGGCCCGGAGCTTTTCTCTCAAGTTTGTCTGCTCT 2152
OY 758 CACACTAATGTGTGTGGGGGTGACTCCAGCTCCTGTAGTCCCTTGGGCTCCACTCA 817
DB 2153 CACACTAATGTGTGGGGGTCTGATTTCC-----AGTCCCTGGCTCCACTCA 2202
OY 818 GGTAGAACCGGAGAGTCTCTCCCTCCGCTCAGAGACTAGAACTTTCCAAAGAAATAGA 877
DB 2203 GGTAGAGCCCAAGAGTCTCTCTCT-CCCCACTCAGAGACTGAACTTTCCAAAGAAATAGA 2261
OY 878 GATTATCCCAAGTCCCGTGTCCAGGCTGTGTGGGTTCTGTCTCTCTCCCAACC 937
DB 2262 GATTATCCCAAGTCTGTGTGTCCAGGCTGTGTGGGTTCTGTCTCTCTCCCAACC 2321
OY 938 CAGTATCTGTGATCTTATGATGTGTCACATCCAGTGTGCTGTGATCCATGAG 997
DB 2322 CAGTATCTGTGATCTTATGATGTGTCACAT-GGGTCTGTGTGGGTTTCCATGAG 2379
OY 998 AGATGCAAAAGTCTTGAATTTTCTGACTTCTCTTTCAGACCCGCCCAAGACACAGCTGA 1057
DB 2380 GAGTGCAAAAGTCTGAAATTTTCTGACTTTC--TCAGATCTTCCAAAGACACAGCTTG 2436
OY 1058 CCCACACCCCTGTCTTGTACTATAGGCGCACCCCTGAGAGTCTGTGGGCTCTGTAC 1117
DB 2437 CCCACACCCCTGTCTGTACCATAGGCGCACCCCTGAGAGTCTGTGGGCTCTGTAC 2496
OY 1118 CTGGGAGATCATGTGACTGTGCGAGCGGATGGGAGAGACCAACCCAGAGCTGGAGC 1177
DB 2497 CTGGGAGATCATGTGACTGTGCGAGCGGATGGGAGAGAACACACAGAGACAGAGC 2556
OY 1178 TCGTGGAGACAGGCTCTCAGGGGATGGAACCTTCCAGAGTGGGAGCTGTGTGTC 1237
DB 2557 TTTGTGAGACAGGCTCTCAGGGGATGGAACCTTCCAGAGTGGGAGCTGTGTGTC 2616
OY 1238 CTTCGGAGAGAGACGAGATACAGCTGTCCATGTGACAGATGAGGGGCTGCGGAGCC 1297
DB 2617 CTTCGGAGAGAGACGAGATACAGCTGTCCATGTGACAGAGAGGCTGCGGAGCC 2676
OY 1298 TCATCTGATGATGAGTAAAGAGGAGAT-----GGAGGATCATGT 1339
DB 2677 TCATCTGATGATGAGGATGAGGAGATGGGTAAGAGAGGAGAGGAGGCTCATGTCT 2736
OY 1340 CTGTTAGGGAAGACAGAGACCTCTCTGAAGACCTTAAACAGGCTGGTGTGAGAGGCTGG 1399
DB 2737 TTTCTGAGGGAAGACAGAGACCTCTCTGAGGCTTTCACAGAGGCTGAGGCTGG 2796
OY 1400 GGGTCAGAGACCTCACCTTCACCTCTTCCAGAGAGTCTTCCCTGCCACCATCC 1459
DB 2797 AATACAGGCGCCCTTACCTCTCTTCCCTTCCAGAGAGTCTTCCACCATCATCC 2856
OY 1460 CATCATGGGTATGTTGCTGAGGCTGTGTCTTCCAGAGAGTCTTCCCTGCCACCATCC 1519
DB 2857 CATCGTGGGATGTTGCTGAGGCTGTGTCTTCCAGAGAGTCTTCCCTGCCACCATCC 2916
OY 1520 CGCTGTGTGTGTGAGAAAGAAAGAGCTCAGTAAAGAGGGGAGCAAGGGGCTGTG 1579
DB 2917 CGCTGTGTGTGTGAGAAAGAAAGAGCTCAGT-AGGAAGGGGTGAGAGTGGAGTGTG 2975
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DB 2976 AGTTTCTGTCTCCACTGGGGGTTTCAAGCCCAAGTAGAATGTGCCCTGCTCATTAAC 3035
OY 1640 TGGGAAGACCATTCACACTCATAGGCTTACAGGCTGTGGGCTGTGTGTGCAAGACTT 1699
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OY 1700 CTCTTTTGAAGACACTCTGACAAATGAAGAGACAGATTTATTAATGATGATGTAGTG 1759

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QY 1875 CCTGGGCTGCAGTACACATTTCTGAAACTTCTCAGGGTCCCAACACTAAGAGTCC 1934
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RESULT 13
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DT 22-OCT-2001 (first entry)
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DE Human polynucleotide SRO ID NO 352.
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KW cerebroprotective; neurotropic; neuroprotective; antibacterial; vituicide;
KW fungicide; ophthalmological; cytostatic; immunosuppressive; neurotropic;
KW neuroprotective; antidiabetic; hepatotropic; antidiabetic;
KW antineoplastic; antidiabetic; antineoplastic; antineoplastic; antibacterial;
KW antiparasitic; cardiac; gene therapy; cancer; immune disorder;
KW cardiovascular disorder; neurological disease; infection; human; ds.
OS Homo sapiens.
XX
XX WO200155308-A2.
PN
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DR	WPI: 2001-488781/53.
XX	New isolated nucleic acids and polypeptides, useful for diagnosing,
PT	treating and/or preventing human diseases and disorders -
XX	
PS	Disclosure: SEQ ID NO 352; 664bp + Sequence Listing; English.
XX	
CC	The invention relates to human polynucleotides (AA163803-AA164012) and
CC	the encoded proteins (AA164497-AA164660) useful for preventing, treating
CC	or ameliorating medical conditions e.g. by protein or gene therapy. The
CC	genes were isolated from a range of human tissues disclosed in the
CC	specification. The nucleic acids, proteins, antibodies and (ant)agonists
CC	are useful in the diagnosis, treatment and prevention of: (a) cancer,
CC	e.g. breast and ovarian cancer and other cancers of the adrenal gland,
CC	bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
CC	urogenital; (b) immune disorders e.g. Addison's disease, allergies,
CC	autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
CC	Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC	colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC	(d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC	epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC	and parasitic infections.
CC	Note: The sequence data for this patent did not form part of the
CC	printed specification, but was obtained in electronic format directly
CC	from WIPO at ftp.wipo.int/pub/published_ptc_sequences.
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 XX (HUMA-) HUMAN GENOME SCI INC.
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 XX Rosen CA, Barash SC, Ruben SM,
 PI WPI; 2001-488781/53.
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 PT New isolated nucleic acids and polypeptides, useful for diagnosing,
 PT treating and/or preventing human diseases and disorders -
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 XX Disclosure; SEQ ID NO 383; 664pp + Sequence Listing; English.
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 CC The invention relates to human polynucleotides (AA163803-AA164012) and
 CC the encoded proteins (AA163497-AA163600) useful for preventing, treating
 CC or ameliorating medical conditions e.g. by protein or gene therapy. The
 CC genes were isolated from a range of human tissues disclosed in the
 CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
 CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
 CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
 CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
 CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
 CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
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Oy	1587	TTCGCCACATCGGGGGTTTAAACCCAGGTGAAGTGCTGCCTCCTGTTACTGGGAG	1646
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Oy	1647	CACCATCACACATCATGAGGGGCTACCCAGGCTGGG - CCCTGTGTGCCAGACCTTCTCTT	1705
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Oy	1766	ACC - TGAATCCAGTAATACACAGGTGAGAGAAAGTCCCCTGCTAAGGACAGACTTAAGA	1824
Db	2363	TCTTGAATTCAGATATTCAATGATCAGGGGAAGTTCCT - GCTAAGACAGACTTAAGA	2421
Oy	1825	GGGCAGTTGGTCAGAGACCACATCTGCTTTCTTTCTTTTTCGTATCGCCCTGGGTCTG	1884
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Oy	2125	TCTCCTGTGCTCTGACCAAGT - GCTGTTTTTGTGTTCTACTAGGCAAGTACAGTGGCC	2183
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Oy	2244	TGGGTTTGAAGGAGACAGGGGACATAGCTGTGCTATAGAGTTTCTTGACTTAAATGT	2303
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Oy	2304	ATTGACAGATGTATGGGCTGTTTAAAGTGCACCCCTCACTGTGACTGATATGAATTGT	2363
Db	2862	TTGCAATGTGTGTAGCTGTTCACAGATGTATCACTTACATGATGACCTGAAATTTGT	2921
Oy	2364	TCAATAAT - TTTTGTGTAGTGAACAGCTGCCCTGTGTGGAGTGAAGTGGCAAGA	2421
Db	2922	TCAATGACTATGTGTTGTGTGAGCCGAGAGAGCTG - CCTGTGGGACGTGAAGATGCAGA	2980
Oy	2422	TTTGTTCATGCTTCCTCTTG 2442	
Db	2981	TTTCTTCACACTTTCCTTG 3001	

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Job time : 798 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 22:09:14 ; Search time 4763 Seconds
(without alignments)
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Percent score: 2442
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Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 49582208

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Listing first 45 summaries

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SUMMARIES

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4	2418.4	99.0	2441	24	US-09-622-846-19
5	1768.4	72.4	4465	17	US-09-359-922-598
6	1768.4	72.4	4465	17	US-09-359-922-598
7	1768.4	72.4	4465	34	US-09-919-002-598
8	1694.4	69.4	4000	40	US-10-102-524-1722
9	1694.4	69.4	4000	40	US-10-102-524-1722
10	1648.2	67.5	5030	33	US-09-881-797-3590
11	1648.2	67.5	5030	38	US-10-021-698-3590
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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23 1554 63.6 3098 36 US-09-950-083-9747 Sequence 9747, Ap
24 1554 63.6 3098 39 US-10-091-572-573 Sequence 573, App
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34 1439.6 59.0 3840 36 US-09-971-429B-10 Sequence 10, App1
35 1431.2 58.6 32768 65 US-60-213-178-223 Sequence 223, App
36 1423 58.3 3357 1 PCT-US01-01309-352 Sequence 352, App
37 1423 58.3 3357 1 PCT-US02-09188-1621 Sequence 1621, App
38 1423 58.3 3357 1 PCT-US02-09370-1713 Sequence 1713, App
39 1423 58.3 3357 1 PCT-US02-09922-1059 Sequence 1059, App
40 1423 58.3 3357 36 US-09-950-082-2079 Sequence 2079, App
41 1423 58.3 3357 40 US-10-105-299-7273 Sequence 7273, App
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ALIGNMENTS

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RESULT 1
US-09-622-846-16
: Sequence 16, Application US/09622846
: GENERAL INFORMATION:
: APPLICANT: National University of Ireland, Cork
: TITLE OF INVENTION: HIV Linked Pre-Exposure and Miscarriage Susceptibility
: TITLE OF INVENTION: Gene
: FILE REFERENCE: P197/PCT
: CURRENT APPLICATION NUMBER: US/09/622, 846
: CURRENT FILING DATE: 2001-07-10
: PRIOR APPLICATION NUMBER: IE980134
: PRIOR FILING DATE: 1998-02-25
: PRIOR APPLICATION NUMBER: IE980668
: PRIOR FILING DATE: 1998-08-12
: NUMBER OF SEQ ID NOS: 23
: SOFTWARE: Patent Ver. 2.1
: SEQ ID NO 16
: LENGTH: 2442
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-622-846-16

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Query Match 100.0%; Score 2442; DB 24; Length 2442;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	2281	TGAGGTTCTTGAATCAATGTATTGATGATGATGGAGTGGTCTTAAAGTGTCAACCCCT	2340
QY	2341	CACGTGACATGATGATTTGTTTCATGAATATTTTCTGTAGTGTGAACAGCTGCCT	2400
Db	2341	CACGTGACATGATGATTTGTTTCATGAATATTTTCTGTAGTGTGAACAGCTGCCT	2400
QY	2401	GTGTGGAGCTGAGTGGCAAGATTTGTTCTATGCTTCCCTTTG 2442	
Db	2401	GTGTGGAGCTGAGTGGCAAGATTTGTTCTATGCTTCCCTTTG 2442	

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RESULT 2
US-09-622-846-17
; Sequence 17, Application US/09622846
; GENERAL INFORMATION:
; APPLICANT: National University of Ireland, Cork
; TITLE OF INVENTION: HLA Linked Pre-Eclampsia and Miscarriage Susceptibility
; TITLE OF INVENTION: Gene
; FILE REFERENCE: PL977PCT
; CURRENT APPLICATION NUMBER: US/09/622,846
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: IE980134
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: IE980668
; PRIOR FILING DATE: 1998-08-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 17
; LENGTH: 2442
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-622-846-17

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Query Match	99.9%;	Score 2440.4;	DB 24;	Length 2442;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2441;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;
QY 1	TACTCCGAGTCCGGGTCGGGATCCACCCCGAGCGCGGAGACCCCGACACCTTC	60		
Db 1	TACTCCGAGTCTCCGGGTCGGGATCCACCCCGAGCGCGGAGACCCCGACACCTTC	60		
QY 61	TACCTGGAGAACCCCAAGGCGCCTTTACCAAAATCCCGGGGTCGGGCGAGGG	120		
Db 61	TACCTGGAGAACCCCAAGGCGCCTTTACCAAAATCCCGGGGTCGGGCGAGGG	120		
QY 121	CGAGGCTCGGTGGGCGGGTCGACGCGAGGGGGTGGGGCCAGGTTCACACCTCCAGTG	180		
Db 121	CGAGGCTCGGTGGGCGGGTCGACGCGAGGGGGTGGGGCCAGGTTCATATCCTCCAGTG	180		
QY 181	GATGATTGCGTCGACCTGGGGTCGACGCGACCCCTCTCCGGGGTATGAACAGTATGC	240		
Db 181	GATGATTGCGTCGACCTGGGGTCGACGCGACCCCTCTCCGGGGTATGAACAGTATGC	240		
QY 241	CTACGATGGCAAGGATTACTCGCCCTGAAACGAGACCTCGCTCTTGACCGCACCGGA	300		
Db 241	CTACGATGGCAAGGATTACTCGCCCTGAAACGAGACCTCGCTCTTGACCGCACCGGA	300		
QY 301	CACGCGGGCTCAGATCTCCAAAGCGCAAGTGTGAGGGCGCCAAATGTGGCTGAACAAAGAG	360		
Db 301	CACGCGGGCTCAGATCTCCAAAGCGCAAGTGTGAGGGCGCCAAATGTGGCTGAACAAAGAG	360		
QY 361	AGCCTACCTGTGAGGGCAAGTCGCTGAGTGGCTCCACATACCTGGAGAACGGGAAGGA	420		
Db 361	AGCCTACCTGTGAGGGCAAGTCGCTGAGTGGCTCCACATACCTGGAGAACGGGAAGGA	420		
QY 421	GATCCTCAGCGCGGGGTACAGGGGCAAGGGGCGCTCCGATCTCTGTAGACCT	480		
Db 421	GATCCTCAGCGCGGGGTACAGGGGCAAGGGGCGCTCCGATCTCTGTAGACCT	480		
QY 481	CTCAGCCTGGCCTAGCAACAAGGAGAGGAAAAATGGGACCAACACTAGATATCGCCT	540		
Db 481	CTCAGCCTGGCCTAGCAACAAGGAGAGGAAAAATGGGACCAACACTAGATATCGCCT	540		
QY 541	CCCTCTGGTCTGAGGGAGAGGAATCCTCTCGGGTTTCCAGATCTCTTACCAGAGATGA	600		
Db 541	CCCTCTGGTCTGAGGGAGAGGAATCCTCTCGGGTTTCCAGATCTCTTACCAGAGATGA	600		
QY 601	TTTCGAGGGCCCGTCGCTCTCTGGGCAATTAAGGATGAATCTCTGAGGAGTGA	660		
Db 601	TTTCGAGGGCCCGTCGCTCTCTGGGCAATTAAGGATGAATCTCTGAGGAGTGA	660		
QY 661	GGGGAAGCAATCCCTGGAAAGCTGATCAGGGGTTCCTTTGACCCCAAGACGCTTGG	720		

Db 661 GGGGAGACAAATCCCTGGAGACTGATCAGGGGTTCCCTTGAACCCACAGACGCTTGG 720
 QY 721 CACGAGACTTTTCCCTGAGGCTTGTCTCTGCTCAGACACATGTTGTGGGGGTC 780
 Db 721 CACGAGACTTTTCCCTGAGGCTTGTCTCTGCTCAGACACATGTTGTGGGGGTC 780
 QY 781 TGACTCCAGCTCCTGAGTCCCTTGGCTCAGTCAAGTCAAGACCGAGTCCCTGCT 840
 Db 781 TGACTCCAGCTCCTGAGTCCCTTGGCTCAGTCAAGTCAAGACCGAGTCCCTGCT 840
 QY 841 CCCCCGCTCAGAGACTGAACTTTCAGAGATAGAGATATCCAGGTGCGCGGTGC 900
 Db 841 CCCCCGCTCAGAGACTGAACTTTCAGAGATAGAGATATCCAGGTGCGCGGTGC 900
 QY 901 AGGCTGTGTGGGTTCTGTGCTCCCTTCCACCCAGGTATCTGTTCTTAAAG 960
 Db 901 AGGCTGTGTGGGTTCTGTGCTCCCTTCCACCCAGGTATCTGTTCTTAAAG 960
 QY 961 ATGCTCAGTCCAGAGTCTGTGAGTCCATGAGAGATGCAAGTGTGAATTTTC 1020
 Db 961 ATGCTCAGTCCAGAGTCTGTGAGTCCATGAGAGATGCAAGTGTGAATTTTC 1020
 QY 1021 TGACTCTTCTTCAAGCCCTCCAGACACACAGTCAACCCCTCTTGTGACTAT 1080
 Db 1021 TGACTCTTCTTCAAGCCCTCCAGACACACAGTCAACCCCTCTTGTGACTAT 1080
 QY 1081 GAGGCTCAGCTGAGTGTGGGCTGGGCTTACCTGAGAGATGCAATGACTGAG 1140
 Db 1081 GAGGCTCAGCTGAGTGTGGGCTGGGCTTACCTGAGAGATGCAATGACTGAG 1140
 QY 1141 CAGCGGAGTGGGAGACACAGACCCAGAGAGTGTGAGAGACAGGCTGTGAGG 1200
 Db 1141 CAGCGGAGTGGGAGACACAGACCCAGAGAGTGTGAGAGACAGGCTGTGAGG 1200
 QY 1201 GATGAGACCTTCCAGAGTGGGAGAGTGTGTGCTCTTCCAGAGAGAGAGATAC 1260
 Db 1201 GATGAGACCTTCCAGAGTGGGAGAGTGTGTGCTCTTCCAGAGAGAGAGATAC 1260
 QY 1261 ACCTGACATGTGACATGAGAGGGGCTGCGAGCCCTCATGCTGAGATGAGTAAAG 1320
 Db 1261 ACCTGACATGTGACATGAGAGGGGCTGCGAGCCCTCATGCTGAGATGAGTAAAG 1320
 QY 1321 GGAATATGAGGACATGCTGTGAGGAGAAAGAGAGGCTCTCTGAAACCTTTAAACG 1380
 Db 1321 GGAATATGAGGACATGCTGTGAGGAGAAAGAGAGGCTCTCTGAAACCTTTAAACG 1380
 QY 1381 GGTGGTGTGAGGGGTGAGGGGTGAGAGACCTTCACTTCACTTCCAGAGACT 1440
 Db 1381 GGTGGTGTGAGGGGTGAGGGGTGAGAGACCTTCACTTCACTTCCAGAGACT 1440
 QY 1441 CTTCCCTGCTCCACCATCCTCATGATGCTGTGCTGCTGCTGCTGCTGCTGCTG 1500
 Db 1441 CTTCCCTGCTCCACCATCCTCATGATGCTGTGCTGCTGCTGCTGCTGCTGCTG 1500
 QY 1501 TAGTCACATGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
 Db 1501 TAGTCACATGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
 QY 1561 GGGTACAGTGGGGTGTGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
 Db 1561 GGGTACAGTGGGGTGTGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
 QY 1621 GTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
 Db 1621 GTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
 QY 1681 CCGTGTGTGAGACCTTCTCTTTTGAAGACCTGTGACATGAGAGAGATTTAT 1740
 Db 1681 CCGTGTGTGAGACCTTCTCTTTTGAAGACCTGTGACATGAGAGAGATTTAT 1740
 QY 1741 TACTTGTATGTTTGTATGATGAGGAGACCTGATCCAGATATACAGGTGAGAGGTC 1800
 Db 1741 TACTTGTATGTTTGTATGATGAGGAGACCTGATCCAGATATACAGGTGAGAGGTC 1800

QY 1801 CTTGGCTAAGAGACACCTTAGAGGGGAGTTGTGTCAGAGACCCACATGCTTCTTGG 1860
 Db 1801 CTTGGCTAAGAGACACCTTAGAGGGGAGTTGTGTCAGAGACCCACATGCTTCTTGG 1860
 QY 1861 TTTTCTGATGCGCCCTGGGCTGTGAGTCAACATTTTCTGGAATCTTCTGAGGTCCTAA 1920
 Db 1861 TTTTCTGATGCGCCCTGGGCTGTGAGTCAACATTTTCTGGAATCTTCTGAGGTCCTAA 1920
 QY 1921 GACTAGAGGTTCTCTAGAGACCTCATGAGCCCTGACACTTCTGCTGCTGCTGCTGCTG 1980
 Db 1921 GACTAGAGGTTCTCTAGAGACCTCATGAGCCCTGACACTTCTGCTGCTGCTGCTGCTG 1980
 QY 1981 TTTTCTTCCACAGATTTGAAAGAGAGAGTCTCTAGGCTGCAAGTATGATGAAG 2040
 Db 1981 TTTTCTTCCACAGATTTGAAAGAGAGAGTCTCTAGGCTGCAAGTATGATGAAG 2040
 QY 2041 AGGCTGATCCCTGAGATCCCTTGGGATCTTGTGTTGGAGGACATGAGGAGCTACCCAC 2100
 Db 2041 AGGCTGATCCCTGAGATCCCTTGGGATCTTGTGTTGGAGGACATGAGGAGCTACCCAC 2100
 QY 2101 CCGACATTTCTCTCTGCGCACATCTCTGTGTCTGTGACAGAGTCTGTTTGTTC 2160
 Db 2101 CCGACATTTCTCTCTGCGCACATCTCTGTGTCTGTGACAGAGTCTGTTTGTTC 2160
 QY 2161 TACTCTAGGAGTACAGTGTGCGGAGGCTCTAATGCTCTCAGGCTGTGAAATGTA 2220
 Db 2161 TACTCTAGGAGTACAGTGTGCGGAGGCTCTAATGCTCTCAGGCTGTGAAATGTA 2220
 QY 2221 CACCCGCGGGGCTGTATGTGTGGTGTGAGGGGAACAGGGAGACATGCTGTGTA 2280
 Db 2221 CACCCGCGGGGCTGTATGTGTGGTGTGAGGGGAACAGGGAGACATGCTGTGTA 2280
 QY 2281 TGAAGTTCTTGTGACTTCAATGATGATGAGCATGTGATGAGGCTTTAAAGTGTACCCCT 2340
 Db 2281 TGAAGTTCTTGTGACTTCAATGATGATGAGCATGTGATGAGGCTTTAAAGTGTACCCCT 2340
 QY 2341 CACTGTACTGATATGAAATTTGTTCATGAAATATTTTCTGTAGTGTGAACAGCTGCTCT 2400
 Db 2341 CACTGTACTGATATGAAATTTGTTCATGAAATATTTTCTGTAGTGTGAACAGCTGCTCT 2400
 QY 2401 GTGTGGAGTGTGAGGAGATTTGTCATGAGGCTTCCCTTGG 2442
 Db 2401 GTGTGGAGTGTGAGGAGATTTGTCATGAGGCTTCCCTTGG 2442

RESULT 3
 US-09-622-846-18
 : Sequence 18, Application us/09622846
 : GENERAL INFORMATION:
 : APPLICANT: National University of Ireland, Cork
 : TITLE OF INVENTION: HLA Linked Pre-Eclampsia and Miscarriage Susceptibility
 : FILE OF INVENTION: Gene
 : FILE REFERENCE: PL977PCY
 : CURRENT APPLICATION NUMBER: US/09/622,846
 : PRIOR FILING DATE: 2001-07-10
 : PRIOR APPLICATION NUMBER: IE980134
 : PRIOR FILING DATE: 1998-02-25
 : PRIOR APPLICATION NUMBER: IE980668
 : NUMBER OF SEQ ID NOS: 23
 : SOFTWARE: Patent In Ver. 2.1
 : SEQ ID NO 18
 : LENGTH: 2441
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 US-09-622-846-18

Query Match 99.1%; Score 2420; DB 24; Length 2441;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACTCCGAGTCTCCGGGCTGTGGAGTCAACCCGAGGCGGAGACCCGACCAACCTTC 60

|||||
Db 1 TACTCCCGAGTCTCCGGGTCTGGGATCCACCCGAGGCCGGGAGCCCGCCAGACCTTC 60
Oy 61 TACTGGGAGAACCCCAAGGGCCCTTACCAAAATCCCCGGGGTGGGTCCGGGCGAGGG 120
Db 61 TACTGGGAGAACCCCAAGGGCCCTTACCAAAATCCCCGGGGTGGGTCCGGGCGAGGG 120
Oy 121 CGAGGCTCGGTGGGGGGGTGACCGAGGGGGTGGGCCAGGTTCTCACACCTCCAGTG 180
Db 121 CGAGGCTCGGTGGGGGGGTGACCGAGGGGGTGGGCCAGGTTCTCACACCTCCAGTG 180
Oy 181 GATGATTGGCTGCACCTGGGGGTCCGAGGAGCCCTCCGGGGATGAAAGATATGC 240
Db 181 GATGATTGGCTGCACCTGGGGGTCCGAGGAGCCCTCCGGGGATGAAAGATATGC 240
Oy 241 CTACGATGGCAAGGATTACCTGCGCTGAACGAGAGACCTGGCTCTTGAGCCGAGCGGA 300
Db 241 CTACGATGGCAAGGATTACCTGCGCTGAACGAGAGACCTGGCTCTTGAGCCGAGCGGA 300
Oy 301 CACTGCGGCTCAGATCTCCAAAGCCAGTGAGGCGGCCAATGTGCTGAACAAGAG 360
Db 301 CACTGCGGCTCAGATCTCCAAAGCCAGTGAGGCGGCCAATGTGCTGAACAAGAG 360
Oy 361 AGCCTACTGGAGGCGACGTGCTGAGAGTGGCTCCACAGATACCTGGAGAACGGGAAGA 420
Db 361 AGCCTACTGGAGGCGACGTGCTGAGAGTGGCTCCACAGATACCTGGAGAACGGGAAGA 420
Oy 421 GATGCTGAGGCGCGGGGTACCAAGGGGCAGTGGGGCGCTCCGTATCTCTGTAGACCT 480
Db 421 GATGCTGAGGCGCGGGGTACCAAGGGGCAGTGGGGCGCTCCGTATCTCTGTAGACCT 480
Oy 481 CTCAGCCTGGGCTACACAGAGAGAGGAGAAATGGGACCAACACTGAGTATTCGCCCT 540
Db 481 CTCAGCCTGGGCTACACAGAGAGAGGAGAAATGGGACCAACACTGAGTATTCGCCCT 540
Oy 541 CCTCTGGGCTGAGGAGAGAAATCTCTGGGTTTCCAGATCTCTGACAGAGATGA 600
Db 541 CCTCTGGGCTGAGGAGAGAAATCTCTGGGTTTCCAGATCTCTGACAGAGATGA 600
Oy 601 TTCTGAGGGCCGCTCCTGCTCTCTGGGACATTAAGGATGAAGTCTGAGGAGATGA 660
Db 601 TTCTGAGGGCCGCTCCTGCTCTCTGGGACATTAAGGATGAAGTCTGAGGAGATGA 660
Oy 661 GGGGAAGACAATCCCGGAAGACTGATCAGGGGTTCCCTTGAACCCACAGCAGCCTTGG 720
Db 661 GGGGAAGACAATCCCGGAAGACTGATCAGGGGTTCCCTTGAACCCACAGCAGCCTTGG 720
Oy 721 CACAGAGACTTTTCCCTCAGGCTTGTCTCTGCTCACACTCAATGTGTGGGGTGC 780
Db 721 CACAGAGACTTTTCCCTCAGGCTTGTCTCTGCTCACACTCAATGTGTGGGGTGC 780
Oy 781 TGACTCAGCTCTCTGAGTCCCTTGGCTCCACACTAGGTCAGAACCCGAGGTCCTGCT 840
Db 781 TGACTCAGCTCTCTGAGTCCCTTGGCTCCACACTAGGTCAGAACCCGAGGTCCTGCT 840
Oy 841 CCCCCGCTCAGAGACTAGAACTTTTCCAGGAATAGAGATTATCCAGGTGCCCCGTGCC 900
Db 841 CCCCCGCTCAGAGACTAGAACTTTTCCAGGAATAGAGATTATCCAGGTGCCCCGTGCC 900
Oy 901 AGGCTGATCTGTGGGTTCTGTGCTCCCTTCCACCCAGATATCTGTTCACTTCTAGG 960
Db 901 AGGCTGATCTGTGGGTTCTGTGCTCCCTTCCACCCAGATATCTGTTCACTTCTAGG 960
Oy 961 ATGGTCACATCCAGGTCGCTGGAGTCCCATGAGAGATGCAAGGTCTTAATTTTC 1020
Db 961 ATGGTCACATCCAGGTCGCTGGAGTCCCATGAGAGATGCAAGGTCTTAATTTTC 1020
Oy 1021 TGACTCTTCTTCAGACCCCGCCAAAGACACAGTGAACCCACCTGTCTTTGACTAT 1080
Db 1021 TGACTCTTCTTCAGACCCCGCCAAAGACACAGTGAACCCACCTGTCTTTGACTAT 1080
Oy 1081 GAGGCCACCTGAGGTCTGTGGGCTTCTACCTCGGAGATCATACGACCTGG 1140
|||||

Db 1081 GAGGCCACCTGAGGTGCTGGGCCCTTGAGGCTTCTACCTCGGAGATCATACGACCTGG 1140
Oy 1141 CAGCGGATGGGAGAGACCAAGACCTGAGACCTGTGGAGACCAAGGCTTCAGAG 1200
Db 1141 CAGCGGATGGGAGAGACCAAGACCTGAGACCTGTGGAGACCAAGGCTTCAGAG 1200
Oy 1201 GATGAACTCTCAGAAAGTGGGACGTGTGTGTCCTTCTGAGAGAGACAGAGATAC 1260
Db 1201 GATGAACTCTCAGAAAGTGGGACGTGTGTGTCCTTCTGAGAGAGACAGAGATAC 1260
Oy 1261 ACSTGCCATGTGCAGCATGAGGAGGCTGCGGAGACCCCTCATGCTGAGATGAGATAGAG 1320
Db 1261 ACSTGCCATGTGCAGCATGAGGAGGCTGCGGAGACCCCTCATGCTGAGATGAGATAGAG 1320
Oy 1321 GAGATGAGAGGCAATCAATGCTGTTAGGAAAGCAGGAGCCCTCTGAAACCTTTAACAG 1380
Db 1321 GAGATGAGAGGCAATCAATGCTGTTAGGAAAGCAGGAGCCCTCTGAAACCTTTAACAG 1380
Oy 1381 GGTGCGTGTGAGAGGCTGGGGGTCCAGAGACCTTCACCTTCCTTCCAGAGCACT 1440
Db 1381 GGTGCGTGTGAGAGGCTGGGGGTCCAGAGACCTTCACCTTCCTTCCAGAGCACT 1440
Oy 1441 CTTCCCTGCCACCATCCCATGATGGGTATCGTTGCTGGCTGTGCTTGGCTTGGAGCTG 1500
Db 1441 CTTCCCTGCCACCATCCCATGATGGGTATCGTTGCTGGCTGTGCTTGGAGCTG 1500
Oy 1501 TACTGACTGAGGCTGGGGTGGCTGCTGTGCTGTGGAGAAAGAGACCTCAGTAAAGAG 1560
Db 1501 TACTGACTGAGGCTGGGGTGGCTGCTGTGCTGTGGAGAAAGAGACCTCAGTAAAGAG 1560
Oy 1561 GGGTGACAAAGTGGGGTGTGAGTTCCTTGTGCCACGTGGGGTTTCAAGCCCGAGTAAAG 1620
Db 1561 GGGTGACAAAGTGGGGTGTGAGTTCCTTGTGCCACGTGGGGTTTCAAGCCCGAGTAAAG 1620
Oy 1621 GTGTGCCCTGCGGTGTACTGAGGAGACCAATCCATGAGGAGGCTTACCGAGCTGG 1680
Db 1621 GTGTGCCCTGCGGTGTACTGAGGAGACCAATCCATGAGGAGGCTTACCGAGCTGG 1680
Oy 1681 CCTGTGTGCGAGCAGCTTCTCTTTGTAAAGCAGCTGTGACAAATGAGAGACAGATTTAT 1740
Db 1681 CCTGTGTGCGAGCAGCTTCTCTTTGTAAAGCAGCTGTGACAAATGAGAGACAGATTTAT 1740
Oy 1741 TACTTGTATGTTGTAGTATGGGAGCTGATGCCAATCAGAGGTCAGGAGAGGTC 1800
Db 1741 TACTTGTATGTTGTAGTATGGGAGCTGATGCCAATCAGAGGTCAGGAGAGGTC 1800
Oy 1801 COTGGCTAAGGACAGACTTGTAGAGGAGTGTGTCGAGAGCCCAACATCTGCTTCTTG 1860
Db 1801 COTGGCTAAGGACAGACTTGTAGAGGAGTGTGTCGAGAGCCCAACATCTGCTTCTTG 1860
Oy 1861 TTTTCTGTATCGCCCTGGGTCTGCAATCAGACATTTCTGGAACCTTCTGAGGGTCCAA 1920
Db 1861 TTTTCTGTATCGCCCTGGGTCTGCAATCAGACATTTCTGGAACCTTCTGAGGGTCCAA 1920
Oy 1921 GACTAGGAGTTCCCTGAGACCTCATGGCCCTGCACTTGTGGCTCTCAAGAGCA 1980
Db 1921 GACTAGGAGTTCCCTGAGACCTCATGGCCCTGCACTTGTGGCTCTCAAGAGCA 1980
Oy 1981 TTTTCTCCACAGATTGAAAAAGAGAGGAGTACTCTCAGGCTGCAAGTAAGTAAAG 2040
Db 1981 TTTTCTCCACAGATTGAAAAAGAGAGGAGTACTCTCAGGCTGCAAGTAAGTAAAG 2040
Oy 2041 AGGCTGATCCCTGAGATCTTGGATCTTGTGTTGGAGCCATGAGGAGCTTCAACCCAC 2100
Db 2041 AGGCTGATCCCTGAGATCTTGGATCTTGTGTTGGAGCCATGAGGAGCTTCAACCCAC 2100
Oy 2101 CCGACAATTCGTCGTCGAGATCTCTGTGGTCTGACAGAGTCTGTGTTTGTTC 2160
Db 2101 CCGACAATTCGTCGTCGAGATCTCTGTGGTCTGACAGAGTCTGTGTTTGTTC 2160
Oy 2161 TACTTAAAGCAGTGAAGTGCAGGCTCTAATGTGTCTCAAGGCTTGTAAATGTGA 2220
Db 2161 TACTTAAAGCAGTGAAGTGCAGGCTCTAATGTGTCTCAAGGCTTGTAAATGTGA 2220
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Db 1501 TAGTCACTGGAGCTGCGGTGCTGCTGCTGTGGAGAAAGAGCTCAGTAGGAAG 1560
Qy 1561 GGGTACAAAGTGGGGTCTGAGTTTTTCTGTCACACTGGGGGTTTCAAGCCCCAGTAGAA 1620
Db 1561 GGGTACAAAGTGGGGTCTGAGTTTTTCTGTCACACTGGGGGTTTCAAGCCCCAGTAGAA 1620
Qy 1621 GTGTGCCCTGCTGTACTGTGGGAAGCACCATCCACACTCATGTGGGCTTACCACCTGGG 1680
Db 1621 GTGTGCCCTGCTGTACTGTGGGAAGCACCATCCACACTCATGTGGGCTTACCACCTGGG 1680
Qy 1681 CCCGTGTGGCAGACCTCTCTTTTGTAAAGCACCTGTGACAAATGGAAGACAGATTTAT 1740
Db 1681 CCCGTGTGGCAGACCTCTCTTTTGTAAAGCACCTGTGACAAATGGAAGACAGATTTAT 1740
Qy 1741 TACCTTGATGATTTAGTATGGGAGCTGATCCAGTAATCAGAGTCAAGAGAGAGTTC 1800
Db 1741 TACCTTGATGATTTAGTATGGGAGCTGATCCAGTAATCAGAGTCAAGAGAGAGTTC 1800
Qy 1801 CCTGGCTAAGGACAGACCTTAGAGAGGAGATTGGTCGAGAGACCCACATCTGTTCTTTC 1860
Db 1801 CCTGGCTAAGGACAGACCTTAGAGAGGAGATTGGTCGAGAGACCCACATCTGTTCTTTC 1860
Qy 1861 TTTTCTCGATGCGCCCTGGGTCTGAGTACACACATTTCTGAAACTTCTCGAGGGTCCAA 1920
Db 1861 TTTTCTCGATGCGCCCTGGGTCTGAGTACACACATTTCTGAAACTTCTCGAGGGTCCAA 1920
Qy 1921 GACTAGAGAGTTCCTTAGAGACCTATGGCCCTGCCACTTTCTGGCTCTCACAGGACA 1980
Db 1921 GACTAGAGAGTTCCTTAGAGACCTATGGCCCTGCCACTTTCTGGCTCTCACAGGACA 1980
Qy 1981 TTTTCTCCACAGATTTGAAAGAGAGAGTACTCTCAGGCTGCAAGTAAGTATGAAG 2040
Db 1981 TTTTCTCCACAGATTTGAAAGAGAGAGTACTCTCAGGCTGCAAGTAAGTATGAAG 2040
Qy 2041 AGGCTGATCCCTGAGATCTTGGGATCTTGTGTTTGGAGACCATGGGGAGCTCACCCAC 2100
Db 2041 AGGCTGATCCCTGAGATCTTGGGATCTTGTGTTTGGAGACCATGGGGAGCTCACCCAC 2100
Qy 2101 CCCACAAATTCCTGCTGGCCACATCTCCTGCTGCTGAGCAGAGTGTGTTTTTGTTC 2160
Db 2101 CCCACAAATTCCTGCTGGCCACATCTCCTGCTGCTGAGCAGAGTGTGTTTTTGTTC 2160
Qy 2161 TACTTAGGAGTGAAGTGGCCAGGCTTAATGTGTCTCAGCGCTTGTAAATGTGA 2220
Db 2161 TACTTAGGAGTGAAGTGGCCAGGCTTAATGTGTCTCAGCGCTTGTAAATGTGA 2220
Qy 2221 CACCCCGGGGGGCTGATGTGTGGGTGTTGAGGGGAACAGGGACATAGCTGTGCTA 2280
Db 2221 CACCCCGGGGGGCTGATGTGTGGGTGTTGAGGGGAACAGGGACATAGCTGTGCTA 2280
Qy 2281 TGAAGTTCTTGTGACTTCATGTATTGAGCATGTGATGGGCTTTTAAAGTGCACCCCT 2340
Db 2281 TGAAGTTCTTGTGACTTCATGTATTGAGCATGTGATGGGCTTTTAAAGTGCACCCCT 2340
Qy 2341 CACTGTGACTGATATGAATTTGTTCAATGAATTTTTCTGTAGTGTGAACAGCTGCCCT 2400
Db 2341 CACTGTGACTGATATGAATTTGTTCAATGAATTTTTCTGTAGTGTGAACAGCTGCCCT 2400
Qy 2401 GTGTGGAGCTGATGGGCAAG 2420
Db 2401 GTGTGGAGCTGATGGGCAAG 2420

RESULT 5
US-09-359-922-598
; Sequence 598, Application US/09359922
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; TITLE OF INVENTION: LIBRARIES
; FILE REFERENCE: 20411-752CON1
; CURRENT APPLICATION NUMBER: US/09/359, 922
; CURRENT FILING DATE: 1999-07-22
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EARLIER APPLICATION NUMBER: US 09/205,155
; EARLIER FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 13203
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 598
; LENGTH: 4465
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-359-922-598

Query Match 72.4%; Score 1768.4; DB 17; Length 4465;
Best Local Similarity 86.2%; Pred. No. 0;
Matches 2126; Conservative 0; Mismatches 281; Indels 59; Gaps 13;

Qy 5 CCCAGTCTCCGGGTCTGGGATCCACCCCGAGCCCGGAGCCCGCCAGACCTCTACC 64
Db 1079 CCACAGTCTCCGGGTCTGGGATCCAGATCCGCCCGAGCCCGGAGCC--CCGAGACCTCTGGCC 1136
Qy 65 TGGAGAAACCCCAAGGCGCTTTAC-----AAAATCCCCC 101
Db 1137 CGGAGAGAGGCCCAAGGCGCTTTACCGGTTTCAATTTTCAAGTTTAGGCCAATAATCCCCCC 1196
Qy 102 GGGTGGTCCGGGCGAGAGGCGAGGCTGGTGGGCGGCGGTGACCGAGGGGTGGGCGAG 161
Db 1197 GGGTGGTCCGGGCGG-6GGCGGGCTCGGGGAGCGGGCTGACCGCGGGGTGGGCGAGT 1255
Qy 162 GTTCTCACACCCCTCAGTGTGATGTGGTGCAGCTGGGGGTCCGACGAGCGCTCTCTC 221
Db 1256 GTTCTCACACCATCAAGTATGTATGTATGTGGTGCAGCTGGGGGTCCGAGCGGCGCTCTC 1315
Qy 222 GCGGATATGAACAGTATGCTTACATGAGGCAAGATTACCTCGCCCTGAAGAGAGACCTGC 281
Db 1316 GCGGATATGAGAGAGAGAGAGAGAGGCAAGATTACATGAGGCTTACAGAGAGAGAGCTGC 1375
Qy 282 GCTCTGAGACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 341
Db 1376 GCTCTGAGACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1435
Qy 342 ATGTGGCTGAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 401
Db 1436 ATGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1495
Qy 402 ACCGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 461
Db 1496 ACCGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1555
Qy 462 CCTGATCTCTGTAGACCTCTCAGCGCTTAGCACAAGAGAGAGAGAGAGAGAGAGAGAG 521
Db 1556 CCTGATCTCTGTAGATCTCCCGGCTGGCTCCCAAGAGAGAGAGAGAGAGAGAGAGAG 1615
Qy 522 AACACTAGATATTCGCCCTCTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 581
Db 1616 AACACTAGATATTCGCCCTCTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1675
Qy 582 ATTCGTGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 641
Db 1676 ATTCGTGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1735
Qy 642 AAGTCTCTGAGGAGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 701
Db 1736 AATCTCTGAAGAGAT-GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1794
Qy 702 GAC-CCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 760
Db 1795 GACACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1854
Qy 761 ACTCAATGTGTGGGGGTCTGACTCCAGCTCCTGAGTGTGCTGCTGCTGCTGCTGCTGCTG 820
Db 1855 ACTCAATGTGTGGGGGTCTGACTCCAGCTCCTGAGTGTGCTGCTGCTGCTGCTGCTGCTG 1914
Qy 821 CAGACCGAGAGTCTCTGCTCCCGCTCAGAGAGTCAAGAGTTCACAGAGATAGAGAGAT 880
Db 1915 CAGAGCCAGAGATGCTGCTGCTCCTC-TTCAGAGAGATGAATTTTCCAGGAGATAGAGAT 1973
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QY 881 TATCCAGAGTGCCGCTGTCAGAGCTGGGCTTCTGGCTCCCTTCCACCCAG 940
 DB 1974 TATCCAGAGTGCCGCTGTCAGAGCTGGGCTTCTGGCTCCCTTCCACCCAG 2033
 QY 941 GTATGAGTCTTCTTATGAGTGTACATCCAGAGTCTCTGTGATGTCCATGAGA 1000
 DB 2034 GTGTCCTGCTTCTTATGAGTGTACATCCAGAGTCTCTGTGATGTCCATGAGA 2091
 QY 1001 TGCAGAGTCTTCTTATGAGTGTACATCCAGAGTCTCTGTGATGTCCATGAGA 1060
 DB 2092 TGCAGAGTCTTCTTATGAGTGTACATCCAGAGTCTCTGTGATGTCCATGAGA 2151
 QY 1061 ACCACCTGCTTCTTATGAGTGTACATCCAGAGTCTCTGTGATGTCCATGAGA 1120
 DB 2152 ACCACCTGCTTCTTATGAGTGTACATCCAGAGTCTCTGTGATGTCCATGAGA 2211
 QY 1121 CGAGATCATCTGATCCGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 1180
 DB 2212 CGAGATCATCTGATCCGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 2271
 QY 1181 TGGAGACAGGCTTGCAGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 1240
 DB 2272 TGGAGACAGGCTTGCAGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 2331
 QY 1241 CTGGAGAGGAGCAGAGTATACAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 1300
 DB 2332 CTGGAGAGGAGCAGAGTATACAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 2391
 QY 1301 TGTGAGATGAGTATGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 1360
 DB 2392 CCTGAGATGAGTATGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 2451
 QY 1361 TGTGAGATGAGTATGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 1420
 DB 2452 TGTGAGATGAGTATGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 2491
 QY 1421 ACCTGCTTCCAGAGAGTCTTCCAGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 1480
 DB 2492 ACCTGCTTCCAGAGAGTCTTCCAGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 2551
 QY 1481 CCTGCTGCTTCCAGAGAGTCTTCCAGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 1540
 DB 2552 CCTGCTGCTTCCAGAGAGTCTTCCAGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 2611
 QY 1541 GAAAGAGTCTGAGTATGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 1600
 DB 2612 GAAAGAGTCTGAGTATGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 2671
 QY 1601 GTTTCAGAGGAGTATGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 1660
 DB 2672 GTTTCAGAGGAGTATGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 2731
 QY 1661 ATGGGCTTCCAGAGAGTCTTCCAGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 1720
 DB 2732 ATGGGCTTCCAGAGAGTCTTCCAGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 2791
 QY 1721 ACAATGAGGAGTATGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 1780
 DB 2792 ACAATGAGGAGTATGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 2850
 QY 1781 TCACAGGAGTATGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 1840
 DB 2851 TCACAGGAGTATGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 2908
 QY 1841 ACCGAGTATGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 1898
 DB 2909 ACCGAGTATGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 2968
 QY 1899 TGGAGAGTCTGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 1958
 DB 2969 TGGAGAGTCTGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 3028

QY 1959 CTTCGAGGCTTCCAGAGAGTCTTCCAGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 2018
 DB 3029 CTTCGAGGCTTCCAGAGAGTCTTCCAGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 3088
 QY 2019 AGCTGCAAGTATGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 2078
 DB 3089 AGCTGCAAGTATGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 3148
 QY 2079 AG-CCATGAGGAGGAGTATGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 2137
 DB 3149 AGCCATGAGGAGGAGTATGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 3208
 QY 2138 CTGACAGGAGTCTGAGTATGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 2197
 DB 3209 CTGACAGGAGTCTGAGTATGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 3268
 QY 2198 TCTCTGAGGAGTATGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 2257
 DB 3269 TCTCTGAGGAGTATGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 3328
 QY 2258 GAACAGGAGGAGTATGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 2317
 DB 3329 GAACAGGAGGAGTATGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 3388
 QY 2318 GGGCTGTTTAAAGTATGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 2375
 DB 3389 GGGCTGTTTAAAGTATGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 3448
 QY 2376 TTTGATGATGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 2435
 DB 3449 TTTGATGATGAGGAGGAGTGGAGGAGCAGACCCAGAGTGTGAGCTGG 3508
 QY 2436 CCCTT 2441
 DB 3509 TCCTT 3514
 RESULT 6
 US-09-359-922-598
 : Sequence 598, Application US/09359922A
 : GENERAL INFORMATION:
 : APPLICANT: Leshkowitz, Dena
 : TITLE OF INVENTION: NOVEL CONFIGS OBTAINED FROM VARIOUS CDNA
 : FILE REFERENCE: 20411-752CON1
 : CURRENT FILING DATE: 1999-07-22
 : EARLIER FILING DATE: 1998-12-03
 : EARLIER APPLICATION NUMBER: US 09/034,341
 : EARLIER FILING DATE: 1998-12-03
 : NUMBER OF SEQ ID NOS: 13203
 : SOFTWARE: FASTSEQ for Windows Version 3.0
 : SEQ ID NO 598
 : LENGTH: 4465
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : US-09-359-922-598
 Query Match 72.4%; Score 1768.4; DB 17; Length 4465;
 Best Local Similarity 86.2%; Pred. No. 0;
 Matches 2126; Conservative 0; Mismatches 281; Indels 59; Gaps 13;
 QY 5 CCCAGTCTCCGGGCTGAGATCCACCCGAGGAGCCGCGGAGCCCGCAGACCTCTAC 64
 DB 1079 CCACAGTCTCCGGGCTCGAATCCGCGGAGGAGCCGCGGAGCC--CCGAGACCTTGGCC 1136
 QY 65 TGGAGAACCCCAAGGCGCTTACC-----AAATCCCGCC 101
 DB 1137 CGGAGAGGCGCAGGCGCTTACCGGTTTATTTTACGTTTAAAGCCAAATAATCCCGCC 1196
 QY 102 GGGTGGGTCGGGCGAGGCGGAGGCTGGTGGGCGGCGTGCACCGAGGAGGCTGGGCGCAG 161

Db	1197	GGGTTGGTCGGGGG-GGCGGGGCTCGGGGACCGGCTACCGCGGGGTCGGGGCCAG	1255
QY	162	GTTCCTACACCCCTCCAGTGAATTTGGCTCGACCTGGGGTCCGACGGACGCTCTCC	221
Db	1256	GTTCACACCATCCAGATATGTATGTATGGCTCGACAGTGGGGTCCGACGGGGCTTCGCC	1315
QY	222	CGGGGTATGAACAGTATCCCTACGATGGCAGAGATTACTCGGCTCGAACAAGAACCTCGC	281
Db	1316	CGGGGTACCGGACCCCTACGACGGCAAGGATTAATGCTGACCTGAAACAAGAACCTCGC	1375
QY	282	GCTCCTGACCGCAGCAGCAGTGGGGCTCGAGATCTCAACAGCGCAAGTGAAGCGGCCA	341
Db	1376	GCTCTTGGACCGCGCGGACATGGCGGCTCGAGTACCAACAGCGCAAGTGGAGCGGCC	1435
QY	342	ATGTGGCTGAACAAGAGAGCTTACCTGAGAGGCGACGTGGTGGATGTGCTCCACAGAT	401
Db	1436	ATGAGCGCGACAGTGTGAGAGCCTTCCGTGATGGCGACGTGGCTGAGTGGCTCCACAGT	1495
QY	402	ACCTGGAGAACGGGAAGAGATGTGACGCGGGGGATACCAAGGGGCACTGGGGGGCTC	461
Db	1496	ACCTGGAGAACGGGAAGAGAGCTGTGACGCGACGCGGATACCAAGGGGCCACGGGGGCTC	1555
QY	462	CCTGATCTCTGTAAACCTCTCAGCCTGAGCCTAGCACAAGAGAGAGAAATGGAGCC	521
Db	1556	CCTGATCGCCTGTAGATCTCCGGGGCTGGCCTCCACAAAGAGGGGAGACAAATTTGGAGCC	1615
QY	522	AACACTAGAAATATCGCCCTCCCTCTGTGCTTGAAGGAAGGAATCCTCGGGTTTCCAG	581
Db	1616	AACACTAGAAATATCGCCCTCCCTCTGTGCTTGAAGGAAGGAATCCTCGGGTTTCCAG	1675
QY	582	ATTCGTGTACCAAGAGTGAATTTCTGAGGGGCCCTCTGCTCTCTGGACAAATTAAGGGATG	641
Db	1676	ATTCGTGTACCAAGAGTGAATTTCTGAGGGTTCCGGCCTGCTCTGACACAAATTAAGGGATA	1735
QY	642	AAAGTCTTGAGGAGTGTGAGGGGAGACAAATCCCTGGAAGACTGATCAGGGTTCCTTT	701
Db	1736	AAATCTCTTAAAGGAAT-GACGGGAAACACATCCCTGAATTAAGATGAATTTGTTCCCTTT	1794
QY	702	GAC-CCCAAGAGCCTTGTGGACACAGAGATTTTCCCTCAGGCGCTTGTCTGCTGCCTCAC	760
Db	1795	GACACCGGAGCTGCTTGGGCCCGTGACTTTTCTCTCAGGCGCTTGTCTGCTGCCTCAC	1854
QY	761	ACTCAATGTGTGGGGGTGTGACTCCACACTCTCTGAGTCCCTTGAGCTCACTAGCT	820
Db	1855	ACTCAATGTGTGGGGGTGTGAGTCCAGACACTTGTAGTCTCTCAGCCTCCACTCAGGT	1914
QY	821	CAGAACCAGAGTCCCTGCTCCCCCGCCCTCAGANACTAAGAACTTCAAGGAATAGAGAT	880
Db	1915	CAGGACCAAGAGTGGCTGTTTCTTC-TTAAGGAACTAAGAAATTTTCAAGGAATAGAGAT	1973
QY	881	TATCCAGAGGCCGATGTCAGGCTGGTGTCTGGGTTGTGTGCTCCCTTCCACCCAC	940
Db	1974	TATCCAGAGGCCGATGATGTCAGGCTGGTGTCTGGGTTGTGTGCTCCCTTCCACCCAC	2033
QY	941	GTAATCTGATTTCTTAGATGTGCATATCCAGGTGCTGCTGGAAGTCCCAATGAGAGA	1000
Db	2034	GTAATCTGATTTCTTCAATATGATGACCAAT--GTGTGCTGGAAGAGTGTCCCAATGAGAGA	2091
QY	1001	TGCAAAATGCTTAAATTTTGTGACTCTTCTTTCAGACCCCCCAACAGACACAGTACC	1060
Db	2092	TGCAAAATGCTTAAATTTTGTGACTCTTCTTTCAGACCCCCCAACAGACATATGACCC	2151
QY	1061	ACCACCTGTCTTGTACTATGAGGCCACCTGAGGTGCTGGGCCCTTGACTCTGACTG	1120
Db	2152	ACCACCTGTCTTGTACTATGAGGCCACCTGAGGTGCTGGGCCCTTGACTCTGACTG	2211
QY	1121	CGGAGATCATACGACCTGGCAGCGGGATGGGGAGACAGACCCAGACAGCTGAGAGCTCG	1180
Db	2212	CGGAGATCATACGACCTGGCAGCGGGATGGGGAGACAGACCCAGACAGGAGCTCG	2271
QY	1181	TGGAGACCGGCTGACAGGGATGGAACCTTTCAGAAAGTGGCAGCTGTGGTGTGCTT	1240

Db	2272	TGGAGACCAGGCTTCAGAGGGATGGAACTTCCAGAAAGTGGGGCGCTGTGTGCTCCCTT	2331
Qy	1241	CTGGAGAGGACACAGATATACACGTGCCATGTGCAGCATGAGGGGCTGCGGAGCCCTCA	1300
Db	2332	CTGGAGAGGACAGAGATACACCTGCCATGTGCGAGCATGAGGGCTGTGCCAAGCCCTCA	2391
Qy	1301	TCCTAGATGGAATGAGGAGGAGATAGGAGCATCATGTCTGTATGGGAAAGAGAGGCC	1360
Db	2392	CCCTAGATGGGGTAAAGGAGGAGATGGGGGTGTGATGTCTTAAAGGAAGCAGAGGCC	2451
Qy	1361	TCCTAGAGACCTTTAAAGAGGGTGGGTGTGAGGGCTGGGGGTCCAGAGCCCTCACCTTC	1420
Db	2452	TCCTAGAGACCTTTAGCA-----GGGTCAAGGGCCCTCACCTTC	2491
Qy	1421	ACCTCCTTTCCACAGACAGCTTTCCTGCTCCACCATATCCCATCATATGGGTATGCTGTGG	1480
Db	2492	CCCTCTTTTCCACAGAGCTGTCTTCCACCCACCATCCCATCTGTGGCATATGTGTGG	2551
Qy	1481	CCGTGGTGTCTTGGAGCTGTAGTCACAGCAGCAGCTGGGTGCTGTGCTGTGGAGAAA	1540
Db	2552	CCTGTCTTCTCTTGGAGCTGTGATCAGTACCTAGAGCTGTGGTGTGCTGCTGTAGTGGAGAG	2611
Qy	1541	GAGAGGCTCAGGTTAAGAAAGGGGTGACAAATGGGGTCTGAATTTCTTGTTCCTACATGGG	1600
Db	2612	GAGAGGCTCAGTGTGAGAAAGGGGTGAAAGGGGTGTGAAATTTCTGTCTCACTGAGG	2671
Qy	1601	GTTTCAAGCCCCAGGTAGAGAGTGTCCCTGCTGGTGTCTGTGGAAAGACATCCACACTC	1660
Db	2672	GTTCACAGCCCCAGTAAATATGTCCCTGTCTCTATTACTGTGGAAAGCACCTTCCACATTC	2731
Qy	1661	ATGGGCTTACCAGCCTGGGGCCTGTGTGTCACAGACCTTCTCTTTTGAAGCACCTGTG	1720
Db	2732	ATGGGCGGACCCAGCCTGGGCCCTGTGTGTCACAGACCTTCTCTTTTGAAGCACCTGTG	2791
Qy	1721	ACATTAAGACAGATTTTATTTACTGTGATGTAGTGTAGTGTGGGGACCTGTATCCAGTAA	1780
Db	2792	AAATTAAGACAGATTTTATTTACTGTGATGTAGTGTAGTGTGGGGACCTGTATCCAGAG	2850
Qy	1781	TCACAGGTGAGGAGAGGTCCCTGGCTAAGACAGACCTTAAAGAGGCGATTTGCTCGAGG	1840
Db	2851	TCACAGTCAACAGG--GGAAGGTCCCTGAGGACAGACCTCAAGAGGGCTATTGTGTCCAGG	2908
Qy	1841	ACCCATATCTGTTTCTCTGTTTTCCTGAT--GGCCCGGGTGTGCAAGTACACATTTTC	1898
Db	2909	ACCCACACCTGTTTCTTATGTGTCTGTATCCCGCCCTGGGTCTGCAATACACATTTTC	2968
Qy	1899	TGGAACCTTCTCGAGGGTCCAGACTAGGAGGTTCTCTAGGACCTCATGGCCCTGCCAC	1958
Db	2969	TGGAACCTTCTCGAGGGTCCAGACTAGGAGGTTCTCTAGGACCTCATGAAGGCCCTGCCCTC	3028
Qy	1959	CTTTTCTGCGCTCTCACAGACATTTTCTTCCACAGATTTGAAGAAGGAGGAGCTACCTC	2018
Db	3029	CTTTCTGTGTCTCACAGGACATTTTCTTCCACAGATTTGAAGAAGGAGGAGCTACCTTC	3088
Qy	2019	AGGCTGCAATAGTATGGAAGAGGCTGATCCCTGAGATCCTTGGGATCTTGTGTTGGG	2078
Db	3089	AGGCTGCAATAGTATGGAAGAGGCTGATCCCTGAGATCCTTGGGATCTTGTGTTGGG	3148
Qy	2079	AG--CCATGGGGAGCTCACCCACCCACACATTTCTCTCTGGCCACATCTCTGTGGTCT	2137
Db	3149	AGCCCAATGGGGAGCTCACCCACCCACCAATTTCTCTCTAGCCACATTTCTGTGGGAT	3208
Qy	2138	CTGACACAGGAGCTTTTCTTCTACTCTTAGGCAAGTACAGTGTGCCAGGGCTCTATGTG	2197
Db	3209	CTGACACAGGTCCTTTTCTTCTTCTACCCAGGCAAGTACAGTGTGCCAGGGCTCTGATGTG	3268
Qy	2198	TCTCTCAGCGCTGTAAATGTGACACCCCGGGGGCTGATGTGTGTGGGTGTGTAAGG	2257
Db	3269	TCTCTCAGCGCTGTAAAGTGTAGAGCTGTGAGGGGCTGATGTGTGTGGGTGTGAGGG	3328
Qy	2258	GAAACAGGGGACATAGCTGTGTCTATGAGCTTCTTTTACCTCAATGATTTAGACATGTGAT	2317
Db	3329	GAAACAGTGTACACAGCTGTGTGTATGGGGTTTCTTTGATTTGGATGTATTTAGACATGTGAT	3388

Db	2612	GAGAGGCTCAGGTGAGAAAGGGGTGAAAGGTTGGGGTCTGAGATTTCTTGTCATGTAGG	2671
Qy	1601	GTTCCTCAAGCCCGCAGGTAGAAAGTGTGCCCTGCCTGGTTACTGGAGACACCATCCACACTC	1660
Ddb	2672	GTTCCTCAAGCCCGCAGGTAGAAATGTGCCCTGTCTCATTTACTGGGAGACACTTCCTCCAAATC	2731
Qy	1661	ATGGGCTCTACCCAGCACTGGGCGCCGTGTGTGCACACACTCTCTTTTGTAAACACTCTGTG	1720
Ddb	2732	ATGGGCGCCAGCCACCTGGGCGCCGTGTGTGCAGCACTTACTCTTTTGTAAACACTCTGT	2791
Qy	1721	ACAAATGAGAGACAGATTATTTATCCCTATGATTTGTAGTATGGGAGCCTGATCCAGTAA	1780
Ddb	2792	AAATATGAGAGACAGATTATTTATCCTTGATTAACGGCGGTGAT--GGAGCTGATCCAGCAG	2850
Qy	1781	TCACAGTTCAGAGACAGAGTCCCTGGCTTAAGSACAGACCTTAAAGAGGCAAGTGTGTGAGG	1840
Ddb	2851	TCACAGTTCAGACAG--GGAAGGTCCCTGAGAGACAGACTTAAAGAGGCAATATGTGTCCAGG	2908
Qy	1841	ACCCACATCTGCTTCCCTGTTTTCCTGAT--CGCCCTGGGTCTGCAGTCACACATTTTC	1898
Ddb	2909	ACCCACACTGCTTCTTCATGTTTCCGTGATCCCGGCCCTGGGTGTGAGTCACACATTTTC	2968
Qy	1899	TGGAACCTTCTCGAGGCTCCAAAGACATAGAGAGTTCTCTTAGACCTCATATGCCCCCTCCAC	1958
Ddb	2969	TGGAACCTTCTCTGGGCTCCAAAGACATAGAGAGTTCTCTTAGACCTTAAAGCCCTCGACTC	3028
Qy	1959	CTTTTCGGCTCTGCACAGACATTTTCTTCCACAGATTGAAAGAGGAGCTACTCTC	2018
Ddb	3029	CTTTTCGGTATCTGCACAGACATTTTCTTCCACAGATAGAAAGAGGAGCTACTCTC	3088
Qy	2019	AGGCTGCAAGATGATGAGAGAGGCTATCCCTGAGATCCTTGGGATCTTGTGTGGG	2078
Ddb	3089	AGGCTGCAAGATGATGAGAGAGGCTATCCCTGAGATCCTTGGGATGTTGTGTGGG	3148
Qy	2079	AG--GCATGGGGGAGCTCACCCACCCCAATTCCTCTGGCCACATCTCTGTGGTCT	2137
Ddb	3149	AGCCCATGGGGAGCTCACCCACCCCAATTTCTCTTAGCCACATCTCTGTGGAT	3208
Qy	2138	CTGACCAAGTGTCTGTTTGTCTACTGTAGGCACTGACAGTCCCGAGGCTCTAATGTG	2197
Ddb	3209	CTGACCAAGTGTCTGTTTGTCTACTGCCAGCACTGACAGTCCCGAGGCTCTGAAATG	3268
Qy	2198	TCCTCTACAGGCTGTAAATGTATACACCCCGGGGGGCGTAGTGTGTGCGCTTGTAGGG	2257
Ddb	3269	TCCTCTACACCTGTAAAGGTATAGCTTGAGGCGCTGATGTGTGTGTGGTGGCG	3328
Qy	2258	GAAACAGGGGACATAGCTGTGCTATGAGGTTCTTTTGACTCTAATGATATGAGATGTAT	2317
Ddb	3329	GAAACAGGGGACACAGCTGTGCTATGAGGTTCTTTTGACTGATATGAGATGTGCAT	3388
Qy	2318	GGGCTGTTTAAAGTGTACCCCTCACTGTGACTGATATGAATTTGCTATATATAA--TTT	2375
Ddb	3389	GGGCTGTTTAAAGTGTACCCCTCACTGTGAGAAATATCAATTTTCTATATAATTTT	3448
Qy	2376	TTCTGTGTGTGAAGACGCTGCCCTGTGTGGGACGTAGTGGCAAGATTGTTCAATGCCCT	2435
Ddb	3449	TTCTATATGTGTGACACAGCTGCCCTGTGTGTGGGACTGAGGCAAGATTGTTCCATGCCCT	3508
Qy	2436	CCCTTT 2441	
Ddb	3509	TCCTTT 3514	
RESULT 8			
PCT-US02-10055-1722			
; Sequence 1722, Application PC/TUS0210055			
; GENERAL INFORMATION:			
; APPLICANT: Corixa Corporation			
; APPLICANT: Algate, Paul A.			
; APPLICANT: Mannion, Jane			
; APPLICANT: Gaiger, Alexander			
; APPLICANT: Gordon, Brian			

	APPLICANT	Harlocker, Susan L.	
	TITLE OF INVENTION	COMPOSITIONS AND METHODS FOR THE	
	TITLE OF INVENTION	THERAPY AND DIAGNOSIS OF KIDNEY CANCER	
	FILE REFERENCE	210121.572PC	
	CURRENT APPLICATION NUMBER	PCT/US02/10055	
	NUMBER OF SEQ ID NOS	1863	
	SOFTWARE	FastSeq for Windows Version 4.0	
	SEQ ID NO	1722	
	LENGTH	4000	
	TYPE	DNA	
	ORGANISM	Homo sapiens	
	PCT-US02-10055-1722		
Query Match	69.4%;	Score 1694.4;	DB 1; Length 4000;
Best Local Similarity	85.4%;	Pred. No. 0;	
Matches 2111;	Conservative	0; Mismatches	286; Indels 75; Gaps 17.
Qy	5	CCCGAGTCTCCGGGTCTGGGATCATCCCGAGGCGCGGGAGACCCGCCACCCCTCTACC	64
Db	1062	CCACAGTCTCCGGGTCTCGAGATCCGCCCGAAGCGCGGAGACC--CCGAGACCTTGGCC	1119
Qy	65	TGGGAGAACCCCAAGGGCGCTTACC-----AAATCCCGC	101
Db	1120	CGGGAGAGGCCACGAGGCCCTTTACCCGGTTTCATTTTCAGTTTAGGCCAAAATATCCCCC	1179
Qy	102	GGGTGGGTCCGGGCGAGGGCGAGGCTGGTGGCGGGGCTGACCGAGGGGTTGGGGCCAG	161
Db	1180	AGCTTGTCGGGGGCGG--GGGCGGGGCTCGGGGAGACCGGGCTGACCCGGGGTCCGGGCGAG	1238
Qy	162	GTTCACACCCCTCAGTGGATGTATGGGCTGGCGACCTGGGGGTCCAGCGAGCCCTCTCC	221
Db	1239	GTTCACACCGTCCAGAGATGTATGGCTGGCGACCTGGGGGTGGAGCTGGGCTCTCC	1298
Qy	222	GGGGGTATGAACAGTATGCTTACGATGGCAGGATTTACTGCGCTTGACACGAGACTGC	281
Db	1299	GGGGGTACCAACAGTACGCTTACGACGGCAGGATTTACTGCCCTCGAAAGAGACCTGC	1358
Qy	282	GCTCTGGACCGCAGCGACCTGGGGCTCAGATCTCCAAAGGCGCAAGTGTGAGGGGCGCA	341
Db	1359	GGCTTTGGACCGCGCGGACATGGCAGCTGACACACACCAAGCAAGTGTGGAGGCGGCC	1418
Qy	342	ATGTGGCTGAACAAAGAGAGCTTACCTGGAGGGGACAGTGCCTGGAGTGGCTCCACAGAT	401
Db	1419	ATGTGGCGGAGCAGTTGAGAGCTTACCTGGAGGGGACAGTGCCTGGAGTGGCTCCAGAT	1478
Qy	402	ACCTGAGAACGGGAGAGATGCTGCAAGCGCGCGGCTTACAGGGGCACTGGGGGCGCTC	461
Db	1479	ACCTGAGAACGGGAGAGAGAGCTGCGACGACACGGGTACAGGGGCGCACGGGGCGCTC	1358
Qy	462	CGTGAATCTCTTACACCTCTCAGCTCGGCGCTTACGACAAAGAGAGGAGGAAATGGGACC	521
Db	1539	CGTGAATCTCTTACATCTCCCGGGCTGGCTCCACAAAGAGAGGAGCAATTTGGGACC	1598
Qy	522	AACACTAGAATATGCGCCCTCCCTTGCTCTGAGGAGAGGAATCTCTGGGTTTCCAG	581
Db	1599	AACACTAGAATATGCGCCCTCCCTTGCTCTGAGGAGAGGAATCTCTGGGTTTCCAG	1658
Qy	582	ATCCTGTACCAGAGATGATTTCTGAGGGCGCGCTCTCTCTGGGACAAATTAAGGATG	641
Db	1659	ATCCTGTACCAGAGATGATTTCTGAGGGTTCGGCCCTCTCTCTGACACAAATTAAGGATA	1718
Qy	642	AAGCTCTGAGGAGTGGAGGAGACAAATCCCTGGAAGACTGATCAGGGGTTCCCTTT	701
Db	1719	AAATCTCTGAAGAAAT--GACGGGAGAGAGATCCTTCGAATATGATGAGTGGTTCCCTTT	1777
Qy	702	GAC-----CCACAGCAGCTTTGGCAGCAGACTTTTCCCTCAGGCGCTTGTCTCTGCG	756
Db	1778	GACACACACAGGAGAGAGCTTTGGGCGCGCTGACATTTTCTCTCAGGCGCTTGTCTCTGCT	1837
Qy	757	TGCACATCATGTGTGGGGGTCTGACCTCAGCTCTCTGAGTCCCTTGGGCTCCACTC	816
Db	1838	TGCACATCATGTGTGGGGGTCTGATCCACGACATTTCTGAGTCCCTTGGGCTCCACTC	1897

Db 1120 CGGAGAGGCCCAAGCGCCTTTACCGGTTTCAATTTTCAATTAGGCCAAAAATCCCCC 1179
QY 102 GGGTGGGTCGCGGAGGAGGAGCTCGGTGGCGGCGCTGACCGAGGGGGTGGGCCAG 161
Db 1180 AGGTTGGTCCGGGGC-GGGCGGGGCTCGGGGGACCGGGCTGACCGGGGGTCCGGGCCAG 1238
QY 162 GTTCTCACACCTTCAGTGGATGTTGGCTCGACCTGGGGTTCGACGGACCTCTCC 221
Db 1239 GTTCTCACACCTTCAGTGGATGTTGGCTCGACCTGGGGTTCGACGGACCTCTCC 1298
QY 222 GCGGATTAACAAGTACCTAGATGGCAAGGATTACCGCGCCCTGAACGAGGACCTGC 281
Db 1299 GCGGATTAACAAGTACCTAGATGGCAAGGATTACCTCGCCCTGAACGAGGACCTGC 1358
QY 282 GCTTCCTGACCGGACGCGACATCGGCTCAGATCTCCACAGGCGCAAGTGTAGGGCGCCA 341
Db 1359 GCTTCCTGACCGGCGGCGGACATGGCAGCTCAGACCAACAAAGCAAGTGGAGCGGCC 1418
QY 342 ATGTGGCTGAACAAGAGAGACCTACCTGGAGGGCACGTGGTGGTGGCTCCACAGAT 401
Db 1419 ATGTGGCGGAGCACTTGAAGCCTACCTGGAGGGCACGTGGTGGTGGCTCCACAGAT 1478
QY 402 ACCTGGAGAACGGGAGAGAGATGTCTGACGCGCGGCTACCAAGGCGAGTGGGGCGCTC 461
Db 1479 ACCTGGAGAACGGGAGAGAGAGATGTCTGACGCGCGGCTACCAAGGCGAGTGGGGCGCTC 1538
QY 462 CCTGATCTCTGTAGACCTCTCAGCCTGGCTGACACAGAGAGAGAGAAATGGGACC 521
Db 1539 CCTGATCTCTGTAGATCTCCCGGGCTGGCTCCACAAAGAGGGGAGACAAATTTGGGACC 1598
QY 522 AACACTAGAAATATGCGCTCCCTCCCTGGTCCGAGAGGAGAGAAATCCCTGGGGTTCCAG 581
Db 1599 AACACTAGAAATATGCGCTCCCTCCCTGGTCCGAGAGGAGAGAAATCTCTCGGGTTTCAG 1658
QY 582 ATCTGTACACAGAGAGTATCTGAGGGCCCGTCTCTCTGTGGAACAATTAAGGATG 641
Db 1659 ATCTGTACACAGAGAGTATCTGAGGGTCCGGCTCTCTGTGGAACAATTAAGGATG 1718
QY 642 AAGTCTGAGGAGTGGAGGGGAAAGACAAATCCCTGGAAACATATAGGGGTTCCCTTT 701
Db 1719 AAGTCTGAGGAGTGGAGGGTCCGGCTCTCTGTGGAACAATTAAGGATG 1777
QY 702 GAC-----CCACACGACGCTTTGGACAGGACTTTTCCCTCGAGGCTTTGTTCTCGCC 756
Db 1778 GACACACACAGGACGACGCTTTGGGCCGCTGACCTTTTCTCTCAGGGCTTTGTTCTCGCT 1837
QY 757 TCACACTCAATGTGTGTGGGGTCTGACTCCAGCTCTGTGATGTTCCCTGGCTTCACCTC 816
Db 1838 TCACACTCAATGTGTGTGGGGTCTGAGTCCAGCACTTGTGATGTTCTGACGCTCCACTC 1897
QY 817 AAGTCAAGAACGGAGTCCCTGCTCCCGGCTCAGAGACTGAATTTCCAAAGGAATAGG 876
Db 1898 AAGTCAAGAACGGAGTCCCTGCTCCCGGCTCAGAGACTGAATTTCCAAAGGAATAGG 1955
QY 877 AGATTATCCAGAGTCCGCTGCTCAGGCTGTGTCTGGGTTCTGTGCTCCCTGCCACC 936
Db 1956 AGATTATCCAGAGTCCGCTGCTCAGGCTGTGTCTGGGTTCTGTGCTCCCTGCCACTC 2015
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Oy 2286 TTTCTTTGATCTCAATGATTTGAGCATGTGATGGGCTGTTTAAAGTCCAGCCCTACTG 2345
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; Sequence 10456, Application PC/TUS0101334
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc., et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC010PCT
; CURRENT APPLICATION NUMBER: PCT/US01/01334
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
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; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
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; PRIOR APPLICATION NUMBER: 60/241,809
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; PRIOR APPLICATION NUMBER: 60/229,509
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 PCT-US01-01339-6712
 : Sequence 6712, Application PC/TUS0101339
 : GENERAL INFORMATION:
 : APPLICANT: Human Genome Sciences, Inc., et al.
 : TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 : FILE REFERENCE: PC006PCT

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? CURRENT APPLICATION NUMBER: PCT/US01/01339
? CURRENT FILING DATE: 2001-03-17
? NUMBER OF SEQ ID NOS: 10231
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 6712
? LENGTH: 3098
? TYPE: DNA
? ORGANISM: Homo sapiens
PCT-US01-01339-6712

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Query Match	63.6%;	Score 1554;	DB 1;	Length 3098;
Best Local Similarity	82.5%;	Pred. No. 0;		
Matches 2047;	Conservative	0;	Mismatches 350;	Indels 83; Gaps 20;

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OY	61	TACCTGGAGAACCCCAAGGCGCCCTTTA-----CCAAATACC	98
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OY	99	CGCGAGGTGGGTCGGGCGGAGGGGAGGCTGGGCGGGCGGGGCGTGAACCGAGGGGGCTGGGGC	158
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OY	159	CAGTTTCTCACACCCTTCACAGTGAATGATGCTGGACCTGGGGTTCGACGGACGCTTC	218
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OY	219	TCCCGGGGTATGAACAGTATGCTTACGATGGCAGAGTATACCTCGCCCGAAGCGAGACC	278
Db	800	TCCCGGGGTATCACACACACGCGTACGAGGGAGGAAATTACATCTCCCGAACGAGACAC	859
OY	279	TGGGCTCTCGAGACCGGACGCGAATCGGGCTCAGATCTCAAGCGCAAGTGTAGGGCG	338
Db	860	TGGCTCTCTGGACCGGGCGGACCGGTGGCTGATGCACCAAGCGCTTATGTAGGGAG	919
OY	339	CCAAATGGCTGAACAAAGGAGAGCCTTACTGGAGGGCACGTGCGCTGAGTGGCTGCACA	398
Db	920	AGGAATATGTCAGAGAGATTTAGAGCACTTACTGGAGGGCGAGTGGCTGGATGCTGCCCA	979
OY	399	GATACCTGGAGAACGGGAAGAGATCTGTGAGCGCGGGGTACAGGGGCAATGGGGGGC	458
Db	980	GATACCTGGAGAAATGGGAAGAGAACGCTACAGCGCGCAAGTACCAAGGGCCAT-GGGGGC	1038
OY	459	CTCCCTGATCTCCTGTAGACCTTTCAGCCTGGCTAGCAAGAGAGAGGAAATGGG	518
Db	1039	CTTCCCATCTCCTGTAGATCTTGTGGATGGCTTCGCAAGAGTGTGGAGAGAAATGTGA	1098
OY	519	ACCAACACTGAATATATGCGCTCCCTGTGATCTGTGAGGAGAGAAATCTCTGGATTC	578
Db	1099	CCCAATGCTAGAAATATGCGCTCCCTCTATGATCTGATGAGAAATCTTCTGGCTTC	1158
OY	579	CAGATCTCTTACAGAGAGATTTCTGAGGGCCGCTCTGCTCTTGGACAAATTAAGG	638
Db	1159	GAGATTCGGTACAGAAAGTGTGAGAGTCCGCGCTGCTCTTGGACAAATTAAGG	1218
OY	639	ATGAAGTCTCTGAGGAGAGTGTGAGGGGAACAATCCTTGAAGACTGATACAGGGTCTCC	698
Db	1219	ATGAATTTCTTGAGGGGAATGGA-GGGAAAGATCCTTGGATATCCGATCCGGGTCTCC	1277
OY	699	TTTGA-CCCCACAGACCTTGGCACACAGACTTTTCCCTTAGGCTTTGTCTCTGCT	757
Db	1278	TTTGAAGCCCTCCAAACACCTTTGGGCCCGGTGACTTTTCTCAAAATTTTGTCTCTGCT	1337
OY	758	CACACTCAATGTGTGTGGGGTCTGACTCAGCTCCTCTGAAATCCCTTGGCTCACATCA	817
Db	1338	CACACTCAATGTGTGTGAGGCTCTGATTC-----ATTCCTCGGCTCCACTTA	1387
OY	818	GGTCAGAACCGAGATCCCTGCTCTCCCGGCTCAGAGACTAGAACTTTCCAAAGAAATAGA	877
Db	1388	GGTCAGAACCGAAGTCCCTGCTCTCCCGC-CTAGAGACTCTAACCTTTCCAAAGAAATAGA	1446

[illegible]

Fri Jan 31 06:07:01 2003

us-09-622-846-16.rpm

Page 23

OY	1935	TCCTGAGACCTCATGGCCCTGCGACACCTTTCTGGCCCTCAGAGCAATTTCTTCCACAG	1994
OY	1935	TCCTGAGACCTCATGGCCCTGCGACACCTTTCTGGCCCTCAGAGCAATTTCTTCCACAG	1994
Db	2531	TCCTGAGACCTCATGGCCCTGCGACACCTTTCTGGCCCTCAGAGCAATTTCTTCCACAG	2580
OY	1995	ATTGAAAGAGAGGAGCTACTCTCAGGCTGCAAGTAACTATGAAGAGAGCTGATCCCTGA	2054
Db	2581	ATTGAAAGAGAGGAGAGCTACTCTCAGGCTGCAAGTAACTATGAAGAGAGCTGATCCCTGA	2639
OY	2055	GATCCCTTGGGATCTCTGTGTGGGAGCC-ATG6GGGAGCTCACCCACCAATTTCTCTC	2113
Db	2640	GATTTGTTGGGATATTGTGTGTCAGGAGCCTATGAGGAGCTCACCCACCAAGTTCTCTC	2699
OY	2114	CTCTGGCAGCATCTCCTGTGCTCTGACACAGTGTCTTTTGTCTTACTCTAGGAGT	2173
Db	2700	-----TAGCCACATCTGTGGGCTCTGACACAGTCTCTTTTGTCTTACCCCAATCACT	2753
OY	2174	GACAGTCCCGAGGGCTCTAATGTGTCTCAGGGCTGTGAAATGAGACGCC-----CGG	2228
Db	2754	GACAGTCCCGAGGGCTCTGAGGGGTCTCTCTCAGAGCTAATTAAGTGCACCTCAGGGCAG	2813
OY	2229	GGGGCCTGATGTGTGTGGTGTGTGAGGG--AACAGGGAGCATAGCTGTGCTATGAGC	2285
Db	2814	GGGGCCTGATGTGTGTGGTGTGTGAGGG--AACAGGGAGCATAGCTGTGCTATGAGC	2873
OY	2286	TTTCTTTGACCTCAATGATATTGAGCAATGTGATGGGCTGTTTAACTGTACCCCMCACTG	2345
Db	2874	TTTCTTTGACCTGTGATGTCTTGAGCAATGAATGGGCTATTTAAGATGTAACTCTACCTG	2933
OY	2346	TGACTGATATGAATTTTGTTCATGAATATTTT--TCTGTACTGTGAAGACAGCTGCCCTGTGT	2404
Db	2934	TGACTGATATGAATTTTGTTCATGAATATTTTCTCTATAGTGTGAAGACAGCTGCCCTGTGT	2993
OY	2405	GGGAGCTAGTGCGCAAGATT 2424	
Db	2994	GGGAGCTAGTGAAGCAAGTAT 3013	

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Job time : 4838 secs

279 TGGGCTCCCTGGACCCGACGGACACTGCGGCTCAGATCTCCAAGCGCAAGTGTGAGCGG

RESULT 2

US-10-203-138A-753/C
Sequence 753, Application US/10203138A

GENERAL INFORMATION:

APPLICANT: Molecular Dynamics, Inc.

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474

FILE REFERENCE: PB 0004 WO 8

CURRENT FILING DATE: US/10/203,138A

PRIOR FILING DATE: 2002-08-02

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 04 February 2000 (04.02.00)

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 26 May 2000 (26.05.00)

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 03 August 2000 (03.08.00)

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 03 October 2000 (03.10.00)

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 27 September 2000 (27.09.00)

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 21 September 2000 (21.09.00)

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 30 June 2000 (30.06.00)

NUMBER OF SEQ ID NOS: 15438

SOFTWARE: Molecular Dynamics Sequence Listing Engine

SEQ ID NO 753

LENGTH: 466

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE: MAP TO AB023057.1

OTHER INFORMATION:

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 4.2

US-10-203-138A-753

Query Match

Best Local Similarity 18.9%; Score 461.2; DB 6; Length 466;

Matches 463; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1103 CCCTGGGCTTCTACCTCGGAGATCATCTGACCTGGCAGCGGATGGGGAGACCA 1162
Db 466 CCCTGGGCTTCTACCTCGGAGATCATCTGACCTGGCAGCGGATGGGGAGACCA 407
QY 1163 CCCAGAGCTGGAGCTCGTGGAGACACAGGCTGCAGGGGATGAGACCTTCCAAAGTGG 1222
Db 406 CCCAGAGCTGGAGCTCGTGGAGACACAGGCTGCAGGGGATGAGACCTTCCAAAGTGG 347
QY 1223 CAGCTGTGTGTGCTTCTGTGAGAGGAGAGATACAGTGCCTATGTGACAGATGAG 1282
Db 346 CAGCTGTGTGTGCTTCTGTGAGAGGAGAGATACAGTGCCTATGTGACAGATGAG 287
QY 1283 GGTGCGGAGGCCCTCATGTGATGAGATGAGTAAGAGGAGAGATGAGAGCATGTCTG 1342
Db 286 GGTGCGGAGGCCCTCATGTGATGAGATGAGTAAGAGGAGAGATGAGAGCATGTCTG 227
QY 1343 TTAGGGAAGACAGAGACCTCTCTGAAGACCTTTAACAAGGTCGGTGTGAGGCTGGGG 1402
Db 226 TTAGGGAAGACAGAGACCTCTCTGAAGACCTTTAACAAGGTCGGTGTGAGGCTGGGG 167
QY 1403 TCAGAGACCTTACCTTACCTCTTCCAGAGACAGTCTCCCTGGCCACATCCCAT 1462
Db 166 TCAGAGACCTTACCTTACCTCTTCCAGAGACAGTCTCCCTGGCCACATCCCAT 107
QY 1463 CATGGGTATGCTTGTGCTGCTGTGCTTGTGCTTGTGCTGCTGCTGCTGCTGCTGCTG 1522
Db 106 CATGGGTATGCTTGTGCTGCTGTGCTTGTGCTTGTGCTGCTGCTGCTGCTGCTGCTG 47

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RESULT 3

US-10-203-138A-754/C
Sequence 754, Application US/10203138A

GENERAL INFORMATION:

APPLICANT: Molecular Dynamics, Inc.

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO

TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474

FILE REFERENCE: PB 0004 WO 8

CURRENT FILING DATE: US/10/203,138A

PRIOR FILING DATE: 2002-08-02

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 04 February 2000 (04.02.00)

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 26 May 2000 (26.05.00)

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 03 August 2000 (03.08.00)

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 03 October 2000 (03.10.00)

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 27 September 2000 (27.09.00)

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 21 September 2000 (21.09.00)

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 30 June 2000 (30.06.00)

NUMBER OF SEQ ID NOS: 15438

SOFTWARE: Molecular Dynamics Sequence Listing Engine

SEQ ID NO 754

LENGTH: 466

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE: MAP TO AB023057.1

OTHER INFORMATION:

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 13

US-10-203-138A-754

Query Match

Best Local Similarity 18.9%; Score 461.2; DB 6; Length 466;

Matches 463; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1103 CCCTGGGCTTCTACCTCGGAGATCATCTGACCTGGCAGCGGATGGGGAGACCA 1162
Db 466 CCCTGGGCTTCTACCTCGGAGATCATCTGACCTGGCAGCGGATGGGGAGACCA 407
QY 1163 CCCAGAGCTGGAGCTCGTGGAGACACAGGCTGCAGGGGATGAGACCTTCCAAAGTGG 1222
Db 406 CCCAGAGCTGGAGCTCGTGGAGACACAGGCTGCAGGGGATGAGACCTTCCAAAGTGG 347
QY 1223 CAGCTGTGTGTGCTTCTGTGAGAGGAGAGATACAGTGCCTATGTGACAGATGAG 1282
Db 346 CAGCTGTGTGTGCTTCTGTGAGAGGAGAGATACAGTGCCTATGTGACAGATGAG 287
QY 1283 GGTGCGGAGGCCCTCATGTGATGAGATGAGTAAGAGGAGAGATGAGAGCATGTCTG 1342
Db 286 GGTGCGGAGGCCCTCATGTGATGAGATGAGTAAGAGGAGAGATGAGAGCATGTCTG 227
QY 1343 TTAGGGAAGACAGAGACCTCTCTGAAGACCTTTAACAAGGTCGGTGTGAGGCTGGGG 1402
Db 226 TTAGGGAAGACAGAGACCTCTCTGAAGACCTTTAACAAGGTCGGTGTGAGGCTGGGG 167
QY 1403 TCAGAGACCTTACCTTACCTCTTCCAGAGACAGTCTCCCTGGCCACATCCCAT 1462
Db 166 TCAGAGACCTTACCTTACCTCTTCCAGAGACAGTCTCCCTGGCCACATCCCAT 107

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Oy	1072	TTTGACATGAGAGCCACCCTGAGGTGTGTGGGCTTCCTACCGGAGACATCA	1133
Db	478	TCGTACATTAAGGCCACCCTGAGTCTGTGGGCTTCCTGAGCTTCAACCTGTGAGATCACA	419
Oy	1132	CTGACCTGGAGAGCGGATGSGGAGAGACCACAACCCAGACACTGTGTGAGACAGG	1199
Db	418	CTGGCCCTGGAGAGGATGTGAGAGACCAACTGTGGGACATGTAGAACTCTTAGAGACCCAG	359
Oy	1192	CTCTCAGAGGATGGAACCTTCCAGAAAGTGGGACGCTGTGTGTGCTCTTGTGGAGAGAG	1257
Db	358	CTCTCAGAGGATGGAACCTTCCAGAAAGTGGGACGCTGTGTGTGCTCTTGTGGAGAGAGAA	299

[illegible]

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OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 22:07:33 ; Search time 103 Seconds
(without alignments)
7270.919 Million cell updates/sec

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Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1415	57.9	6553	1	US-08-522-942-1
2	426.8	17.5	600	3	US-08-577-081A-3
3	334.0	13.9	587	3	US-08-577-081A-9
4	333.8	13.8	575	3	US-08-577-081A-6
5	249.2	10.2	544	3	US-08-577-081A-52
6	238	9.7	4059	2	US-08-564-313-2
7	238	9.7	4059	2	PCP-US94-06069-2
8	238	9.7	4059	2	US-08-564-313-1
9	238	9.7	4059	2	PCP-US94-06069-1
10	232.8	9.5	276	3	US-08-127-954-134
11	232.8	9.5	276	3	US-08-577-081A-40
12	229.6	9.4	276	1	US-08-127-954-111
13	228	9.3	276	1	US-08-127-954-109
14	226.4	9.3	276	1	US-08-127-954-110
15	224.8	9.2	276	1	US-08-127-954-101
16	223.2	9.1	276	1	US-08-127-954-96
17	223.2	9.1	276	1	US-08-127-954-99
18	223.2	9.1	276	1	US-08-127-954-108
19	223.2	9.1	276	1	US-08-127-954-116
20	223.2	9.1	276	1	US-08-127-954-117
21	223.2	9.1	276	1	US-08-127-954-118
22	223.2	9.1	276	1	US-08-127-954-131
23	221.6	9.1	276	1	US-08-127-954-95
24	221.6	9.1	276	1	US-08-127-954-100
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30	221.6	9.1	276	1	US-08-127-954-121	Sequence 121, App
31	221.6	9.1	276	1	US-08-127-954-123	Sequence 123, App
32	221.6	9.1	276	1	US-08-127-954-132	Sequence 132, App
33	221.6	9.1	276	1	US-08-127-954-133	Sequence 133, App
34	220	9.0	276	1	US-08-127-954-97	Sequence 97, App
35	220	9.0	276	1	US-08-127-954-98	Sequence 98, App
36	220	9.0	276	1	US-08-127-954-104	Sequence 104, App
37	220	9.0	276	1	US-08-127-954-115	Sequence 115, App
38	220	9.0	276	1	US-08-127-954-129	Sequence 129, App
39	220	9.0	276	1	US-08-127-954-130	Sequence 130, App
40	218.4	8.9	276	1	US-08-127-954-113	Sequence 113, App
41	218.4	8.9	276	1	US-08-127-954-114	Sequence 114, App
42	218.4	8.9	276	1	US-08-127-954-122	Sequence 122, App
43	218.4	8.9	276	1	US-08-127-954-126	Sequence 126, App
44	218.4	8.9	276	1	US-08-127-954-127	Sequence 127, App
45	218.4	8.9	276	1	US-08-127-954-127	Sequence 127, App

ALIGNMENTS

RESULT 1
US-08-522-942-1
Sequence 1, Application US/08522942
Patent No. 5753442
GENERAL INFORMATION:
APPLICANT: Tyan, Dolly B.
TITLE OF INVENTION: METHOD FOR DETERMINING GENETIC
TITLE OF INVENTION: PRESTIPPOSITION FOR SEMONEGATIVE SPONDYLARTHROPHATHIES AND
TITLE OF INVENTION: PRODUCTS THEREFOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 4365 Executive Drive, Suite 1500
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/522,942
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ramos, Robert T.
REGISTRATION NUMBER: 37,915
REFERENCE/DOCKET NUMBER: P07 33624
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-1995
TELEFAX: 619-546-9392
INFORMATION FOR SEQ. ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6553 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: DNA (genomic)
US-08-522-942-1

Query Match 57.9% Score 1415; DB 1; Length 6553;
Best Local Similarity 79.1% Pred. No. 0;
Matches 1963; Conservative 0; Mismatches 380; Indels 140; Gaps 18;

OY 5 CCCGAGTCTCCGGGTCTGGAGTCC-ACCCGAGGCGCGGAGACCCGCCAGACCTTAC 63
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Db 1215 CCCGAGTCTCCGGGTCTGGAGTCCGCCCGGAGGCGGAGACCCGCCAGACCTTAC 1274

QY	64	CTGAGGAAACCCCAAGGAGGCGCTTTA	-----CCAAATCCCCGC	101
Db	1275	CGGCAGAGACCCCAAGGCGCGCTTTA	-----CCAAATCCCCGC	1334
QY	102	GGGTGGGTCCGGGCGAGGGCGAGGCTCGTGGGGCGGGCTACCGAGGGGG--TGGGGC	159	
Db	1335	GGGTGTGTGGGGGGGGGGGGCGTGGGGGAGCGGGGCTGACCGCGGGGGGAGGGGGC	1394	
QY	160	AGGTTCTCACACCCCTCCAGTGGATGATTTGGCTGCACACCTGGGGGTCCACGCGAGCGCTCT	219	
Db	1395	AGGGTCTCACACCCCTCCAGAAATGATTTGGCTGCACACCTGGGGGTCCACGCGAGCGCTCT	1454	
QY	220	CCCGGGGTATGAAACAGTATGCTATCAGATGGCAAGATTAATCTGGCCCTGTAAGAGGACT	279	
Db	1455	CCCGGGGTATCACACAGGAGCGCTATCACAGGCGCAAGATTAATCTGGCCCTGTAAGAGGACT	1514	
QY	280	GGCGTCTCGAGCCGACGCGACACTGGCGCTAGATTTCCAGCGCAATGTGAGCGGC	339	
Db	1515	GACCTCTCTGAGCCGCGCGGAGCACGCGGCTCGATGCATCCACGAGCAAGTGGGAGCGGC	1574	
QY	340	CAATGTGGGTGAAACAAAGAGAGCGCTACCTGGAGGGCACGTGCTGGAGTGGCTCCACG	399	
Db	1575	CGGTGTGGGAGACGCTGAGAGGCTACCTGGAGGGCGAGTGTGGAGTGGCTCCGACG	1634	
QY	400	ATTACCTGGAGAAACGGGAAGAGATGCTGGAGCGCGCGGGTTCACAGGGGCGATGGGGCGC	459	
Db	1535	ATTACCTGGAGAAACGGGAAGAGAGGCTGACGCGCGCGGGTTCACAGGGGCGATGGGGAGC	1694	
QY	460	TCCCTGATTCCTGTGACCTCTCAGCTTGCGCTAGCACAAGAGAGAGAAATGGGA	519	
Db	1695	TTCCTCCATCTCTATTAAGGTCTCCGGGGATGGGCTCCACAGGAAGAGAGAAATGGGA	1754	
QY	520	CCACACACTAGATTATTCGCGCTCCCTCGTGGCTGAGGAGAGAGATCTCTGGTTTC	579	
Db	1755	TCAAGCCTAGATTATTCGCGCTCCCTCGTGAATGAGATGATGATTTCTCGATTTC	1814	
QY	580	AGATCTGTACAGAGATGATTCTGAGGGGCGCGTCGCTCTGTGGGAATAATTAAGGA	639	
Db	1815	-----TCTGGGGGCGCGCTCTTCTCTGTAGGAATAATTAAGGA	1852	
QY	640	TGAAGTCTGTGAGGAGTGGAGGGGGAACAATCCCTGGAAAGACTGATCAGGGTTCCT	699	
Db	1853	TGACGCTCTGTGAGAAATGGAGGGGGAAGACAGTCCCTAGAAATCTGATCAGGGGTTCCT	1912	
QY	700	TTACACCC-ACAGAGCCTT-GGACACAGAGCTTTTCCCTCAGAGCCTTTTCTCGCT	757	
Db	1913	TTTGACCCCTGCAAGCAGCCTTGGAAACCGAGACTTTTCTCTCAGAGCCTTTTCTCGCT	1972	
QY	758	CACACATATGTGTGGGGGTCTGACATCCAGCTCTCTGATGTCCTTGGGCTCCACCTCA	817	
Db	1973	CACACATATGTGTGGGGGTCTGATTCAGATCCAGCTCTCTGATGATCTTTCCTCAGCTCA	2032	
QY	818	GGTCAGAACCGGAGGTCCCTGCTCCCGCGCTCAGAGACTAGAACTTTCCAAAGAAATAGA	877	
Db	2033	GATCAGAGACCAAAATCCCTG-TTCCCGCTCAGAGACTCAGAACTTTCCAAATAGAGA	2091	
QY	878	GATTATTCAGAGTGGCGCTGTCACAGGATGGATGTCAGGGTCTGTGCTCCCTCCACCC	937	
Db	2092	GATTATTCAGAGTGGCTGCTGTCACAGGATGGATGTCAGGGTCTGTGCTCCCTCCACCC	2150	
QY	938	CAGGTATCTGGTTATTCTTATAGATGGTCAATCCAGTGGCTGTGAGTGTCCATTGAG	997	
Db	2151	CAGGTATCTGGTTATTCTTATAGATGGTCAAT--GGATGGTCTTAAAGTGTCCATTGAG	2208	
QY	998	AGATGCAAGGTCTTGAATTTTCTGACTCTCTCTTTCAGACCCGCCCAACACACAGTGA	1057	
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QY	1058	CCACACACCTCTCTTATGATATGAGGACACCCGATAGGTTGGGGCGCTGGGCTCTTAC	1117	
Db	2269	CCACACACCTCTCTTATGATATGAGGACACCCGATAGGTTGGGGCGCTGGGCTCTTAC	2328	
QY	1118	CTCGGAGATCTACTGACTGGCAGGGGATGGGAGAGACCAACCGAGAGCTGGAC	1177	

Dh	2239	CTGGGAGATATCACTGACCTGGGACGGGATGGGAGAGACCAACTCAGACACTGAGAC	2388
Oy	1178	TCGTGGAGACACAGGCTCTGACGGGATGGAACCTTCCAGAACTGGGACAGCTGTGTGTGC	1237
Dh	2389	TTTGGAAGACACAGACACAGAGAAATGAAACCTTCCAAATGTGGGACAGCTGTGTGTGC	2448
Oy	1238	CTTCTGGAGAGAGACAGAAATACAGCTGCCATGTGTACACTATGAGGGGCTCCCGAAGCCC	1297
Dh	2449	CTTCTGGAGAAAGACAGAGATACATCATGTGCATATGACACTAGAGGGGCTCCGAAACCCC	2508
Oy	1298	TCATGTGATGATGATAGAGAGAGAAAT--GAGAGCAATCATGTGTGTGTGAAAGACAG	1355
Dh	2509	TCACCTGAGATGGGATAGSAGAGGGGATGAGGGGTCAATCTCTTCTCAGSMAAGACG	2568
Oy	1356	GAGCTCTCTGAAGACTTATTAACAGGGTGGGTGTGAGGGCTGGGGGTACAGAACCTTCA	1415
Dh	2569	GAGCCCTTGAGCA-----GGGTGAGGGCCCTTCA	2597
Oy	1416	CCATTCAACCTCTTCTCCAGAGCACTCTCCCTGACCACCAATCCCATCATAGGATATCGTT	1475
Dh	2598	TCATTCCCTCTTCTTCCAGAGCCGCTCTCCACAGTACACCGTCCCATCGTGGSCATATGT	2657
Oy	1476	GTGGGCTGGGTGTCTCTGACGCTGTATGACTAGGAGCTGGGGGTGGTGTGTGTGTGTG	1535
Dh	2658	GTGTGCTTGGCTGTCTTACGAGTTGTGTATGACAGCTGTGTGTGTGTGTGTGTGTGT	2717
Oy	1536	AGAAAGAGAGCTCAGGTAAAGGAAGGGGTGACAAATGGGGTCTGATTTTCTTGTCCAC	1595
Dh	2718	AGGAGGAAGAGCTCAGGTAAAGGAAGGGGGGTAGGGGGTGTGATTTTCTTGTCCAC	2777
Oy	1596	TGGGGGTTTCAAGCCCGAGGTAGAAAGTGTACCCTGTCTGTACTGTGGGAAGCACATCCA	1655
Dh	2778	TGGGGGTTTCAAGCCCGAGGTAGAAAGTGTCTCCTGCTCATTTACTGTGGGAAGCAGCATCA	2837
Oy	1656	CACCTCATGGGCTTACCAGGCTGTGG--CCGTGTGTGCAAGCAACCTTCTTGTGTAAAGA	1714
Dh	2838	CA--CAGGGGCTAACGACGAGCTGGGAGCCGTGTGTGCAACACTTACTTGTGTGTGAGA	2895
Oy	1715	CCGTGTACATGAGAGACATATTTATTCCTGTGATGATTTAGTGTAGTGGGACCTGATCC	1774
Dh	2896	CATGTGACATATGAAGACGAGATGTATACCTGTGTGTGTGTGGGTGGGCTCTCATTC	2955
Oy	1775	CAGTATTCACAGGTGAGGAGAGAGTCCCTGTGGCTGAAGGACACACCTTGTGGAGGGCAGTTGG	1834
Dh	2956	CAGATTCATGTAGTCAAGGGAAGGTCCCT--GCTAAGGACAGCCTTGTAGGAGGCACTTGG	3014
Oy	1835	TCGAGAGACCACATGTGCTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1894
Dh	3015	TCGAGAGACCACATGTGCTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	3074
Oy	1895	TTTTCTGAAACTTTCGAGGGTCCACAGACTGAGAGGTTCCTGTAGACCTCATAGGCCCTG	1954
Dh	3075	CTTCTGGAAATTCCTTTGGGCTCCAAAGAGAGAGGTTCCTCATGAATCTCATAGGCCCTG	3134
Oy	1955	CACGCTTTCGGGCTCTCAGCAGGACATTTTCTCCACAGATTGAAGGAAGGAGGACCTTAC	2014
Dh	3135	CTTCTCTCCAGTCCCTCAGAGGGCAATTTCTTCCACAGGTGAAGAAAGGAGGACCTTAC	3194
Oy	2015	TTCTCAGGCTGCAATGATATGAAAGAGAGCTGATCCCTGATATCTTGGATCTTGTGT	2074
Dh	3195	TTCTCAGGCTGCTGTAAATGTATGTGGG-----	3220
Oy	2075	TGGGAGCCATGGGGAGGCTCAACCCACCACCAATTCCTCTGTGGCACATCTCCTGTGG	2134
Dh	3221	GTGGGAGATGTGAGAGAGCTCAACCCACCCTTAATCTCTCTGT--CCACGCTCTCGGGG	3279
Oy	2135	TTCTGTGACAGAGT	2194
Dh	3280	GTCTGTGACAGAGTCTGT	3339
Oy	2195	GTGTCTCTCAGGGTTGTAAATGTGACACC-----CGGGGGGCTGTATGTG	2241

Db 3340 GTGCTCTCAACAGCTTGAAGGTGAGATTCCTGGGCTCTAGAGTGGTGGGCTGGCAGG 3399
 Oy 2242 TGTGGGTTGTGGAGGGAACAGGACATGCTGTCTATGAGGTTCTTGACTTCAT 2301
 Db 3400 TCTGGGGGTGGGTGGGCACTGAGGACCTGGGTAATGAGATTCCTGATTCGAT 3459
 Oy 2302 GTATTGAGCATGTGATGGCTGTTTAAAGTGTCAACCCCTCAGCTGACATGATATGATTT 2361
 Db 3460 GTTTCGCTGTGTGTGGCTGTTTACATGCTGATCATCTACATGACACTACACCAATTT 3519
 Oy 2362 GTTCATGATAT--TTTCTGTAGTGTGAACAGCTGCCCTGTGTGGAGCTGAGTGGCAA 2419
 Db 3520 GTTCATGATGCTGTTTCTTCTGAGCCTGAGACAGCTGTCTGTGAGGAGCTGAGATGAG 3579
 Oy 2420 GATTGTTCAGCCTTCCCTTTG 2442
 Db 3580 GATTCTTCAGCCTCCCTTTG 3602

RESULT 2

US-08-577-081A-3
 ; Sequence 3, Application us/08577081A
 ; Patent No. 6030775

GENERAL INFORMATION:

APPLICANT: Yang, Soo Young
 APPLICANT: Cereb, Nezh
 TITLE OF INVENTION: Methods and Reagents for Typing HLA
 NUMBER OF SEQUENCES: 84
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Opedahl & Larson
 STREET: 1992 Commerce Street Suite 309
 CITY: Yorktown
 STATE: NY
 COUNTRY: US
 ZIP: 10598
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS DOS
 SOFTWARE: Word Perfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/577,081A
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Larson, Marina T.
 REGISTRATION NUMBER: 32,038
 REFERENCE/DOCKET NUMBER: MSK-P-001-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (914) 245-3252
 TELEFAX: (914) 962-4330
 TELEX:
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 600
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: Genomic DNA
 HYPOTHEICAL: no
 ANTI-SENSE: no
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 ORGANISM: human
 FEATURE:
 OTHER INFORMATION: consensus sequence of intron 3 of the
 OTHER INFORMATION: HLA-A gene
 US-08-577-081A-3

Query Match 17.5% Score 426.8; DB 3; Length 600;
 Best Local Similarity 81.6%; Pred. No. 3.7e-110;
 Matches 493; Conservative 37; Mismatches 65; Indels 9; Gaps 4;
 Oy 438 GTACAGGGGCGAGTGGGGGCTCCCTGATCTCTGTAGACCTCTGAGCTGAGCTGAGCA 497
 Db 1 GTACAGGGGCGAGTGGGGGCTCCCTGATCTCTGTAGACCTCTGAGCTGAGCTGAGCA 60
 Oy 498 CAGGAGAGGAGGAGAAATTAAGGATGAAGTCTGTAGAGAGAGGAGGAGGAGGAGGAGG 557
 Db 61 CAGGAGAGGAGGAGAAATTAAGGATGAAGTCTGTAGAGAGAGGAGGAGGAGGAGGAGG 120
 Oy 558 AGAGAAATCTCTGCTGGGCTTCCAGATCTGTACAGAGAGTGTGAGAGGCGCTCT 617
 Db 121 AGAGAAATCTCTGCTGGGCTTCCAGATCTGTACAGAGAGTGTGAGAGGCGCTCT 180
 Oy 618 GCTCTCTGGGAGAAATTAAGGATGAAGTCTGTAGAGAGAGGAGGAGGAGGAGGAGG 677
 Db 181 GCTCTCTGGGAGAAATTAAGGATGAAGTCTGTAGAGAGAGGAGGAGGAGGAGGAGG 239
 Oy 678 GAAGACTGATCAGGGGCTTCCCTTGAC----CCACAGCAGCCTTGGCAGCAGACTTT 732
 Db 240 GAATACGTATGATGATGCTTCCCTTGACAGACACACAGCAGGAGGAGGAGGAGGAGG 299
 Oy 733 TCCCTCAGAGCTTGTCTGTGCTGCTCAGACTCATGTGTGGGGGTGAGTCTGAGCTC 792
 Db 300 TCCCTCAGAGCTTGTCTGTGCTGCTCAGACTCATGTGTGGGGGTGAGTCTGAGCTC 359
 Oy 793 CTCTGAGTCCCTTGGCCTTCCAGCTCAGTCTGAGAGGAGGAGGAGGAGGAGGAGGAGG 852
 Db 360 TCTGTAGCTCTGAGCTTCCAGCTCAGTCTGAGAGGAGGAGGAGGAGGAGGAGGAGG 418
 Oy 853 GACTGAATCTTCCAGAGATTAAGGATTAATCCAGGAGGAGGAGGAGGAGGAGGAGGAGG 912
 Db 419 GATGAATCTTCCAGAGATTAAGGATTAATCCAGGAGGAGGAGGAGGAGGAGGAGGAGG 478
 Oy 913 GGGTCTGTGCTCCCTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 972
 Db 479 GGGTCTGTGCTCCCTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 538
 Oy 973 AGGTCTGCTGAGAGTGTCCCATGAGAGATGCAATGCTGATTTCTGAGCTTCTCT 1032
 Db 539 --RTGCTGAGGAGTGTCCCATGAGAGATGCAATGCTGATTTCTGAGCTTCTCT 596
 Oy 1033 TCAG 1036
 Db 597 WCAG 600

RESULT 3

US-08-577-081A-9
 ; Sequence 9, Application us/08577081A
 ; Patent No. 6030775

GENERAL INFORMATION:

APPLICANT: Yang, Soo Young
 APPLICANT: Cereb, Nezh
 TITLE OF INVENTION: Methods and Reagents for Typing HLA
 NUMBER OF SEQUENCES: 84
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Opedahl & Larson
 STREET: 1992 Commerce Street Suite 309
 CITY: Yorktown
 STATE: NY
 COUNTRY: US
 ZIP: 10598
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS DOS
 SOFTWARE: Word Perfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/577,081A

Page 4

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01 1025 TCTTCTCTTTCAG 1036
02      ||||| ||||
03 Db      576 TCTTCCCGTCAG 587

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05 RESULT 4
06 US-08-577-081A-6
07 ; Sequence 6, Application US/08577081A
08 ; Patent No. 6030775
09
10 GENERAL INFORMATION:
11
12 APPLICANT: Yang, Soo Young
13
14 APPLICANT: Cered, Nezh
15
16 TITLE OF INVENTION: Methods and Reagents for Typing HLA
17
18 TITLE OR INVENTION: Class I Genes
19
20 NUMBER OF SEQUENCES: 84
21
22 CORRESPONDENCE ADDRESSES:
23
24 ADDRESSEE: Opedahl & Larson
25
26 STREET: 1992 Commerce Street Suite 309
27
28 City: Yorktown
29
30 STATE: NY
31
32 COUNTRY: US
33
34 ZIP: 10598
35
36 COMPUTER READABLE FORM:
37
38 MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
39
40 COMPUTER: IBM compatible
41
42 OPERATING SYSTEM: MS DOS
43
44 SOFTWARE: Word Perfect
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46 CURRENT APPLICATION DATA:
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:      FILING DATE:
:      CLASSIFICATION: 435
:      PRIOR APPLICATION DATA:
:      APPLICATION NUMBER:
:      FILING DATE:
:      ATTORNEY/AGENT INFORMATION:
:      NAME: Larson, Marina T.
:      REGISTRATION NUMBER: 32,038
:      REFERENCE/DOCKET NUMBER: MSK-P-001-US
:      TELECOMMUNICATION INFORMATION:
:      TELEPHONE: (914) 245-3252
:      TELEFAX: (914) 962-4330
:      TELEX:
:      INFORMATION FOR SEO ID NO: 6:
:      SPOURCE CHARACTERISTICS:
:      LENGTH: 575
:      TYPE: nucleic acid
:      STRANDEDNESS: double
:      TOPOLOGY: linear
:      MOLECULE TYPE: Genomic DNA
:      HYPOTHETICAL: no
:      ANTI-SENSE: no
:      FRAGMENT TYPE: internal
:      ORIGINAL SOURCE:
:      ORGANISM: human
:      FEATURE:
:      OTHER INFORMATION: consensus sequence of Intron 3 of the
:      OTHER INFORMATION: HLA-B gene
:      US-08-577-081A-6

Query Match      13.88; Score 335.8; DB 3; Length 575;
Best Local Similarity 76.44; Pred. No. 1.3e-84;
Matches 429; Conservative 28; Mismatches 86; Indels 28; Gaps

QY      438  GTACCAAGGGGCGAGTGGGGGCGCCTCCCTGATCTCCTGTAGACCTTCACCTCGGCGCTAGCA 497
:      ||||||| ||||||| ||||| ||| | : ||||| : |
Db      1      GTACCAAGGGGCGAGTGGGGGCGCCTCCCGCATCTCTTAAGTGGGCGGAGATGSSGTCMA 60
:      ||||||| ||||||| ||||| ||| | : ||||| : |

QY      498  CAAAGGAGAGGAGCAAAATGGGAGCAACACTAGAAATATGCGCCCTCGCTCGGCTCGAGGG 557
:      || ||||| ||||| ||||| ||||| ||||| ||||| ||| |
Db      61  CGAGAGAGAGAGAGAAATGGGATCAGCGCTAGATGTGCGCCTCTTGATGGAGATG 1207
:      || ||||| ||||| ||||| ||||| ||||| ||||| ||| |

Y      558  AGAGGATCTCTCTGGGTTTCACAGATCTGTACACAGAGATGATTCTGAGGCGCCGTCT 617

```



```

CORRESPONDENCE ADDRESS:
ADDRESS: Knobb, Martens, Olson and Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,313
FILING DATE: 01-DEC-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/074,344
FILING DATE: 07-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Israel, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: VICAL.033CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4059 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
IMMEDIATE SOURCE:
CLONE: HLA-B7
US-08-564-313-2

Query Match
Best Local Similarity 9.7%; Score 238; DB 2; Length 4059;
Best Local Similarity 91.0%; Pred. No. 9.3e-57;
Matches 253; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1034 CAGACCCCCCAAGACACAGTGTACCCACCTCTTTGACTATGAGGCCACCTGA 1093
DB 2267 CTGACCCCCCAAGACACAGTGTGTGAGACCCACCTCTTCTGACATGAGGCCACCTGA 2208
QY 1094 GGTGCTGGGCGCTGGCTTACCTGCGAGATCATCTGACCTGCGAGCGGATGGG 1153
DB 2207 GGTGCTGGGCGCTGGCTTACCTGCGAGATCATCTGACCTGCGAGCGGATGGG 2148
QY 1154 AGGACCAACCCAGACAGTGTGTGAGACCCAGGCGCTGAGGAGTGAACCTTCC 1213
DB 2147 AGGACCAACCCAGACAGTGTGTGAGACCCAGGCGCTGAGGAGTGAACCTTCC 2088
QY 1214 AGAAGTGGGCACTGTGTGTGCTTCTGTGAGAGAGCAGAGATACAGTGCATGTC 1273
DB 2087 AGAAGTGGGCACTGTGTGTGCTTCTGTGAGAGAGCAGAGATACAGTGCATGTC 2028
QY 1274 AGCATGAGGGGCTGCGGAGCCCTCATGCTGAGATG 1311
DB 2027 AGCATGAGGGGCTGCGGAGCCCTCATGCTGAGATG 1990

RESULT 7
PCT-US94-06069-2/c
Sequence 2, Application PC/TUS9406069
GENERAL INFORMATION:
APPLICANT: Vical Incorporated
APPLICANT: Regents of the University of Michigan
APPLICANT: Nabel, Elizabeth
```

```

APPLICANT: Nabel, Gary
APPLICANT: Lew, Denise
APPLICANT: Marguel, Magda
TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: Knobb, Martens, Olson and Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06069
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/074,344
FILING DATE: 07-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Israel, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: VICAL.033VPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4059 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
STRAIN: HLA-B7
PCT-US94-06069-2

Query Match
Best Local Similarity 9.7%; Score 238; DB 5; Length 4059;
Best Local Similarity 91.0%; Pred. No. 9.3e-57;
Matches 253; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1034 CAGACCCCCCAAGACACAGTGTACCCACCTCTTTGACTATGAGGCCACCTGA 1093
DB 2267 CTGACCCCCCAAGACACAGTGTGTGAGACCCACCTCTTCTGACATGAGGCCACCTGA 2208
QY 1094 GGTGCTGGGCGCTGGCTTACCTGCGAGATCATCTGACCTGCGAGCGGATGGG 1153
DB 2207 GGTGCTGGGCGCTGGCTTACCTGCGAGATCATCTGACCTGCGAGCGGATGGG 2148
QY 1154 AGGACCAACCCAGACAGTGTGTGAGACCCAGGCGCTGAGGAGTGAACCTTCC 1213
DB 2147 AGGACCAACCCAGACAGTGTGTGAGACCCAGGCGCTGAGGAGTGAACCTTCC 2088
QY 1214 AGAAGTGGGCACTGTGTGTGCTTCTGTGAGAGAGCAGAGATACAGTGCATGTC 1273
DB 2087 AGAAGTGGGCACTGTGTGTGCTTCTGTGAGAGAGCAGAGATACAGTGCATGTC 2028
QY 1274 AGCATGAGGGGCTGCGGAGCCCTCATGCTGAGATG 1311
DB 2027 AGCATGAGGGGCTGCGGAGCCCTCATGCTGAGATG 1990

RESULT 8
US-08-564-313-1
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```
Sequence 1, Application US/08564313
Patent No. 5910488
GENERAL INFORMATION:
APPLICANT: Nabel, Elizabeth
APPLICANT: Nabel, Gary
APPLICANT: Lew, Denise
APPLICANT: Marguet, Magda
TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,313
FILING DATE: 01-DEC-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/074,344
FILING DATE: 07-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: VICAL.033CPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4965 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
IMMEDIATE SOURCE:
CLONE: HLA-B7 and Beta-2
US-08-564-313-1
Query Match 9.7%; Score 238; DB 2; Length 4965;
Best Local Similarity 91.0%; Pred. No. 1e-56;
Matches 253; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
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RESULT 9
PCT-US94-06069-1
Sequence 1, Application PC/TUS9406069
GENERAL INFORMATION:
APPLICANT: Vical Incorporated
APPLICANT: Regents of the University of Michigan
APPLICANT: Nabel, Elizabeth
APPLICANT: Nabel, Gary
APPLICANT: Lew, Denise
APPLICANT: Marguet, Magda
TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06069
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/074,344
FILING DATE: 07-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: VICAL.033VPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4965 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
STRAIN: HLA-B7 and Beta-2
PCT-US94-06069-1
Query Match 9.7%; Score 238; DB 5; Length 4965;
Best Local Similarity 91.0%; Pred. No. 1e-56;
Matches 253; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
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Db 1331 AGAAGTGGGCAAGCTGTGTGTCCTTCTGTGAGAGAGAGATACACATCCATGTAC 1390

Qy 1274 AGCATGAGGGGCTGCCGAGCCCTCATGCTGAGATGG 1311

Db 1391 AGCATGAGGGGCTGCCGAGCCCTCATGCTGAGATGG 1428

RESULT 10

US-08-127-954-134

; Sequence 134, Application US/08127954

; Patent No. 5451512

GENERAL INFORMATION:

APPLICANT: Apple, Raymond J.

APPLICANT: Bugawan, Teodorica L.

APPLICANT: Erlich, Henry A.

TITLE OF INVENTION: Methods and Reagents for HLA Class I A

TITLE OF INVENTION: Locus DNA Typing

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:

ADDRESS: Hoffmann-La Roche Inc.

STREET: 340 Kingsland Street

CITY: Nutley

STATE: New Jersey

COUNTRY: U.S.A.

ZIP: 07110-1199

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/127,954

FILING DATE:

CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:

NAME: Petty, Douglas A.

REGISTRATION NUMBER: 35,321

REFERENCE/DOCKET NUMBER: 8873

TELECOMMUNICATION INFORMATION:

TELEPHONE: (510) 814-2974

TELEFAX: (510) 814-2974

INFORMATION FOR SEQ ID NO: 134:

SEQUENCE CHARACTERISTICS:

LENGTH: 276 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-127-954-134

Query Match 9.5%; Score 232.8; DB 1; Length 276;

Best Local Similarity 90.2%; Pred. No. 7e-56;

Matches 249; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 162 GTTCTCACACCTTCAGTGTGATGTTGGCTGCGACCTGGGGTCCGACGAGCCCTCTCC 221

Db 1 GTTCTCACACCTTCAGTGTGATGTTGGCTGCGACCTGGGGTCCGACGAGCCCTCTCC 60

Qy 222 GCGGATATGAACAGTATGCTTACGATGCGAAGATTACCTCGCCCTGAAGAGAGACTGC 281

Db 61 GCGGATATGAACAGTATGCTTACGATGCGAAGATTACCTCGCCCTGAAGAGAGACTGC 120

Qy 282 GCTCTGACCGCAGCGGACACTGCGCTCAGATCTCCAAAGCGCAAGTGTAGCGGCCA 341

Db 121 GCTCTGACCGCAGCGGACACTGCGCTCAGATCTCCAAAGCGCGCC 180

Qy 342 ATGTGGCTGAACAAAGAGAGAGCTTACCTGAGAGGAGAGCTGCTGAGTGCCTCACAGAT 401

Db 181 GTGTGGCGGAGACGCTAGAGAGCTTACCTGAGAGGAGAGCTGCTGAGTGCCTCACAGAT 240

Qy 402 ACCTGAGAGAGAGAGAGAGTGTGAGAGCGCGG 437

Db 241 ACCTGAGAGAGAGAGAGAGTGTGAGAGCGCGG 276

RESULT 11

US-08-577-081A-40

; Sequence 40, Application US/08577081A

; Patent No. 6030775

GENERAL INFORMATION:

APPLICANT: Yang, Soo Young

APPLICANT: Cereb, Nezh

TITLE OF INVENTION: Methods and Reagents for Typing HLA

TITLE OF INVENTION: Class I Genes

NUMBER OF SEQUENCES: 84

CORRESPONDENCE ADDRESS:

ADDRESS: Opedahl & Larson

STREET: 1992 Commerce Street Suite 309

CITY: Yorktown

STATE: NY

COUNTRY: US

ZIP: 10598

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette - 3.5 inch, 1.44 MB storage

COMPUTER: IBM compatible

OPERATING SYSTEM: MS DOS

SOFTWARE: Word Perfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/577,081A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Larson, Marina T.

REGISTRATION NUMBER: 32,038

REFERENCE/DOCKET NUMBER: MSK-P-001-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (914) 245-3252

TELEFAX: (914) 962-4330

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 276

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

HYPOTHETICAL: no

ANTI-SENSE: no

FRAGMENT TYPE: internal

ORIGINAL SOURCE:

ORGANISM: human

FEATURE:

OTHER INFORMATION: consensus sequence of exon 3 of the

OTHER INFORMATION: nonclassical HLA genes

US-08-577-081A-40

Query Match 9.5%; Score 232.8; DB 3; Length 276;

Best Local Similarity 90.2%; Pred. No. 7e-56;

Matches 249; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 162 GTTCTCACACCTTCAGTGTGATGTTGGCTGCGACCTGGGGTCCGACGAGCCCTCTCC 221

Db 1 GTTCTCACACCTTCAGTGTGATGTTGGCTGCGACCTGGGGTCCGACGAGCCCTCTCC 60

Qy 222 GCGGATATGAACAGTATGCTTACGATGCGAAGATTACCTCGCCCTGAAGAGAGACTGC 281

Db 61 GCGGATATGAACAGTATGCTTACGATGCGAAGATTACCTCGCCCTGAAGAGAGACTGC 120

Qy 282 GCTCTGACCGCAGCGGACACTGCGCTCAGATCTCCAAAGCGCAAGTGTAGCGGCCA 341

Db 121 GCTCTGACCGCAGCGGACACTGCGCTCAGATCTCCAAAGCGCGCC 180

Qy 402 ACCTGAGAGAGAGAGAGTGTGAGAGCGCGG 437

Db 342 ATGTGGCTGAACAAAGAGAGAGCTTACCTGAGAGGAGAGCTGCTGAGTGCCTCACAGAT 401

Db 181 GTGTGGGAGAGAGCTGAGAGCTACTGTGAGGACGACGTGGAGTGGCTCCGAGAT 240
 Oy 402 ACCGTGAGAACGGGAGAGATGCTGACGCGCGG 437
 Db 241 ACTGTGAGAACGGGAGAGATGCTGACGCGCGG 276

RESULT 12

US-08-127-954-111
 ; Sequence 111, Application US/08127954
 ; Patent No. 5451512

GENERAL INFORMATION:

APPLICANT: Apple, Raymond J.
 APPLICANT: Bugawan, Teodorica L.
 APPLICANT: Erlich, Henry A.
 TITLE OF INVENTION: Methods and Reagents for HLA Class I A
 TITLE OF INVENTION: Locus DNA Typing
 NUMBER OF SEQUENCES: 173
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hoffmann-La Roche Inc.
 STREET: 340 Kingsland Street
 CITY: Nutley
 STATE: New Jersey
 COUNTRY: U.S.A.
 ZIP: 07110-1199

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/127,954
 FILING DATE:
 CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:

NAME: Petry, Douglas A.
 REGISTRATION NUMBER: 35,321
 REFERENCE/DOCKET NUMBER: 8873
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (510) 814-2974
 TELEFAX: (510) 814-2977
 INFORMATION FOR SEQ ID NO: 111:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 276 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-127-954-111

Query Match 9.4%; Score 229.6; DB 1; Length 276;
 Best Local Similarity 89.5%; Pred. No. 5.6e-53;
 Matches 247; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Oy 162 GTTCTCACACCTCCAGTGTGATGCTGCGACCTGGGTCGACGAGCCTCTCTCC 221
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 Db 1 GTTCTCACACCTCCAGTGTGATGCTGCGACCTGGGTCGACGAGCCTCTCTCC 60
 Oy 222 GGGGGTATGACATATGCTTACGATGCAAGATTAAGTCTGCAAGAGAGACCTGC 281
 |||||||
 Db 61 GGGGGTATGACATATGCTTACGATGCAAGATTAAGTCTGCAAGAGAGACCTGC 120
 Oy 282 GCTCTGACCGACGAGACGACATGCGGCTCAGATTCACAGGCAAGTGTGAGCGGCCA 341
 |||||||
 Db 121 GCTCTTGGAGCGCGGACATGCGGCTCAGATTCACAGGCAAGTGTGAGCGGCC 180
 Oy 342 ATGTGCTGACAAAGAGAGAGCTTACCTGAGGAGCAGTGGAGTGGCTCCACAGAT 401
 |||||||
 Db 181 ATGTGCTGACAAAGAGAGAGCTTACCTGAGGAGCAGTGGAGTGGCTCCACAGAT 240
 Oy 402 ACCTGAGAGACGGGAGAGATGCTGACGCGCGG 437
 |||||||

Db 241 ACTGTGAGAACGGGAGAGATGCTGACGCGCGG 276

RESULT 13

US-08-127-954-109
 ; Sequence 109, Application US/08127954
 ; Patent No. 5451512

GENERAL INFORMATION:

APPLICANT: Apple, Raymond J.
 APPLICANT: Bugawan, Teodorica L.
 APPLICANT: Erlich, Henry A.
 TITLE OF INVENTION: Methods and Reagents for HLA Class I A
 TITLE OF INVENTION: Locus DNA Typing
 NUMBER OF SEQUENCES: 173
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hoffmann-La Roche Inc.
 STREET: 340 Kingsland Street
 CITY: Nutley
 STATE: New Jersey
 COUNTRY: U.S.A.
 ZIP: 07110-1199

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/127,954
 FILING DATE:
 CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:

NAME: Petry, Douglas A.
 REGISTRATION NUMBER: 35,321
 REFERENCE/DOCKET NUMBER: 8873
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (510) 814-2974
 TELEFAX: (510) 814-2977
 INFORMATION FOR SEQ ID NO: 109:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 276 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-127-954-109

Query Match 9.3%; Score 228; DB 1; Length 276;
 Best Local Similarity 89.1%; Pred. No. 1.6e-54;
 Matches 246; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Oy 162 GTTCTCACACCTCCAGTGTGATGCTGCGACCTGGGTCGACGAGCCTCTCTCC 221
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 Db 1 GTTCTCACACCTCCAGTGTGATGCTGCGACCTGGGTCGACGAGCCTCTCTCC 60
 Oy 222 GGGGGTATGACATATGCTTACGATGCAAGATTAAGTCTGCAAGAGAGACCTGC 281
 |||||||
 Db 61 GGGGGTATGACATATGCTTACGATGCAAGATTAAGTCTGCAAGAGAGACCTGC 120
 Oy 282 GCTCTGACCGACGAGACGACATGCGGCTCAGATTCACAGGCAAGTGTGAGCGGCCA 341
 |||||||
 Db 121 GCTCTTGGAGCGCGGACATGCGGCTCAGATTCACAGGCAAGTGTGAGCGGCC 180
 Oy 342 ATGTGCTGACAAAGAGAGCTTACCTGAGGAGCAGTGGAGTGGCTCCACAGAT 401
 |||||||
 Db 181 ATGTGCTGACAAAGAGAGCTTACCTGAGGAGCAGTGGAGTGGCTCCACAGAT 240
 Oy 402 ACCTGAGAGACGGGAGAGATGCTGACGCGCGG 437
 |||||||
 Db 241 ACTGTGAGAACGGGAGAGATGCTGACGCGCGG 276

RESULT 14
 US-08-127-954-110

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: Sequence 110, Application US/08127954
: Patent No. 5451512
: GENERAL INFORMATION:
: APPLICANT: Apple, Raymond J.
: APPLICANT: Bugawan, Teodorica L.
: APPLICANT: Erlich, Henry A.
: TITLE OF INVENTION: Methods and Reagents for HLA Class I A
: NUMBER OF SEQUENCES: 173
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hoffmann-La Roche Inc.
: STREET: 340 Kingsland Street
: CITY: Nutley
: STATE: New Jersey
: COUNTRY: U.S.A.
: ZIP: 07110-1199
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/127,954
: FILING DATE:
: CLASSIFICATION: 436
: ATTORNEY/AGENT INFORMATION:
: NAME: Pelly, Douglas A.
: REGISTRATION NUMBER: 35,321
: REFERENCE/DOCKET NUMBER: 8873
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (510) 814-2974
: TELEFAX: (510) 814-2977
: INFORMATION FOR SEQ ID NO: 110:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 276 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-127-954-110

Query Match
Best Local Similarity 9.3%; Score 226.4; DB 1; Length 276;
Matches 245; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 162 GTTCTACACCCCTCCAGTATGATGCTGCGACCTGGGCTCCGACGAGCCTCTCC 221
DB 1 GTTCTACACCCCTCCAGTATGATGCTGCGACCTGGGCTCCGACGAGCCTCTCC 60
QY 222 GCGGGTATGAAACAGTATGCTTACGATGCGAAGATTAACCTCGCCCTGAAGAGACCTGC 281
DB 61 GCGGGTATGAAACAGTATGCTTACGATGCGAAGATTAACCTCGCCCTGAAGAGACCTGC 120
QY 282 GCTCTGACACCGGACGACACTGCGCTCAGATCTCAGACGACGACGATGTGAGGGGCGCA 341
DB 121 GCTCTGACACCGGACGACACTGCGCTCAGATCTCAGACGACGACGATGTGAGGGGCGCC 180
QY 342 ATGTGGCTTAAGAAAGAGAGCCTTACCTGAGGGGACAGCTGAGTGCTCCACAGAT 401
DB 181 ATGTGGCTTAAGAAAGAGAGCCTTACCTGAGGGGACAGCTGAGTGCTCCACAGAT 240
QY 402 ACCTGAGAACGGAGAGAGATGCTGCAAGCGCGCG 437
DB 241 ACCTGAGAACGGAGAGAGATGCTGCAAGCGCGCG 276

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RESULT 15

US-08-127-954-101
Sequence 101, Application US/08127954

Patent No. 5451512
GENERAL INFORMATION:
APPLICANT: Apple, Raymond J.
APPLICANT: Bugawan, Teodorica L.

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: APPLICANT: Erlich, Henry A.
: TITLE OF INVENTION: Methods and Reagents for HLA Class I A
: NUMBER OF SEQUENCES: 173
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hoffmann-La Roche Inc.
: STREET: 340 Kingsland Street
: CITY: Nutley
: STATE: New Jersey
: COUNTRY: U.S.A.
: ZIP: 07110-1199
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/127,954
: FILING DATE:
: CLASSIFICATION: 436
: ATTORNEY/AGENT INFORMATION:
: NAME: Pelly, Douglas A.
: REGISTRATION NUMBER: 35,321
: REFERENCE/DOCKET NUMBER: 8873
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (510) 814-2974
: TELEFAX: (510) 814-2977
: INFORMATION FOR SEQ ID NO: 101:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 276 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-127-954-101

Query Match
Best Local Similarity 9.2%; Score 224.8; DB 1; Length 276;
Matches 244; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 162 GTTCTACACCCCTCCAGTATGATGCTGCGACCTGGGCTCCGACGAGCCTCTCC 221
DB 1 GTTCTACACCCCTCCAGTATGATGCTGCGACCTGGGCTCCGACGAGCCTCTCC 60
QY 222 GCGGGTATGAAACAGTATGCTTACGATGCGAAGATTAACCTCGCCCTGAAGAGACCTGC 281
DB 61 GCGGGTATGAAACAGTATGCTTACGATGCGAAGATTAACCTCGCCCTGAAGAGACCTGC 120
QY 282 GCTCTGACACCGGACGACACTGCGCTCAGATCTCAGACGACGACGATGTGAGGGGCGCA 341
DB 121 GCTCTGACACCGGACGACACTGCGCTCAGATCTCAGACGACGACGATGTGAGGGGCGCC 180
QY 342 ATGTGGCTTAAGAAAGAGAGCCTTACCTGAGGGGACAGCTGAGTGCTCCACAGAT 401
DB 181 ATGTGGCTTAAGAAAGAGAGCCTTACCTGAGGGGACAGCTGAGTGCTCCACAGAT 240
QY 402 ACCTGAGAACGGAGAGAGATGCTGCAAGCGCGCG 437
DB 241 ACCTGAGAACGGAGAGAGATGCTGCAAGCGCGCG 276

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Search completed: January 31, 2003, 00:52:52
Job time : 122 secs